

GenCore version 5.1.6
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Run on: September 21, 2004, 12:57:07; Search time 7154 Seconds
(without alignments)
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Perfect score: 1796
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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ALIGNMENTS

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DEFINITION	BD249816	BD249816	33 human	secreted proteins.				
ACCESSION	BD249816	BD249816	33 human	secreted proteins.				
VERSION	BD249816.1	GI:33059586	33 human	secreted proteins.				
KEYWORDS	JP 2002540763-A/18.		33 human	secreted proteins.				
SOURCE	Homo sapiens (human)		33 human	secreted proteins.				
ORGANISM	Homo sapiens		33 human	secreted proteins.				
REFERENCE	1 (bases 1 to 1796)		33 human	secreted proteins.				
AUTHORS	Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R., Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and Komatsoulis,G.		33 human	secreted proteins.				

33 human secreted proteins
 Patent: JP 2002540763-A 18 03-DEC-2002;
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 PN JP 2002540763-A/18
 PD 03-DEC-2002
 PF 08-FEB-2000 JP 2000598519
 PR 10-FEB-1999 US 60/119468
 PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN NI,
 PI DANIEL R SOPPET, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR, HENRIK
 PI S OLSEN,
 PI KIMBERLY A FLORENCE, GEORGE KOMATSOUKIS
 PC C12N15/09, A61K31/7115, A61K38/00, A61K48/00, A61P1/00, A61P1/04,
 PC A61P1/16,
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 Matches 1796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX358786 Sequence 39 from Patent WO0193983.
DEFINITION AX358786
ACCESSION AX358786
VERSION AX358786.1 GI:18675294
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker,K.P., Desnovers,L., Gerritsen,M.B., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K., and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 39 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity 99.6%; Pred. No. 0;
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DEFINITION      Sequence 39 from Patent W00208288.
ACCESSION      AX362279
VERSION      AX362279.1
KEYWORDS      GI:18694597
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ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS      Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Gadowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL      Patent: WO 0208288-A 39 31-JAN-2002;
Genentech, Inc. (US)
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ACCESSION AY358545
VERSION AY358545.1 GI:37182212
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SOURCE Homo sapiens (human)
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Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1837)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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DEFINITION Sequence 55 from Patent WO0112662.
ACCESSION AX083513
VERSION AX083513.1 GI:13185323
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Lal, P., Yue, H., Tang, Y.T., Bandman, O., Burford, N., Azimzai, Y.,
Baughn, M.R., Lu, D.A. and Patterson, C.
TITLE Membrane associated proteins
JOURNAL Patent: WO 0112662-A 55 22-FEB-2001;
Incyte Genomics, Inc. (US)
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AX747710 1785 bp mRNA linear PAT 20-JUN-2003

ACCESSION AX747710
VERSION AX747710.1 GI:32132098
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SOURCE Homo sapiens
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Makamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuko,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1308459-A 1235 07-MAY-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
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VERSION
GI:21751429
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SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
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AUTHORS
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Onura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
TITLE
NEDO human cDNA sequencing project
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1785)
AUTHORS
Isogai, T. and Yamamoto, J.
TITLE
Direct Submission
JOURNAL
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomacshri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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ORIGIN

Query Match 92.8%; Score 1666.2; DB 9; Length 1785;
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RESULT 8
AF251706
LOCUS
DEFINITION Homo sapiens NK inhibitory receptor precursor (NKIR) mRNA, complete cds.
ACCESSION AF251706
VERSION AF251706.1 GI:20330549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1696)
AUTHORS Li, N., Wan, T., Zhang, W. and Cao, X.
TITLE Novel human NK inhibitory receptor NKIR precursor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1696)
AUTHORS Li, N., Wan, T., Zhang, W. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R.China

FEATURES
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Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marudina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,K.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Buttefield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1923)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripoop,S., Thomas,P.J., Touchman,J.W., Tsurgueon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Location/Qualifiers

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RESULT 10
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ACCESSION AY303545
VERSION AY303545.1 GI:31790203
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 956)
Alvarez-Errico, D., Kitzig, F., Sayos, J. and Lopez-Botet, M.
Molecular and functional characterization of IREM-1, a novel
inhibitory receptor expressed by myeloid cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 956)
Alvarez-Errico, D., Kitzig, F., Sayos, J. and Lopez-Botet, M.
Direct Submission
TITLE Submitted (20-MAY-2003) Cexs/Immunology, Universitat Pompeu Fabra,
JOURNAL Doctor Aiguader 80, Barcelona, 08003, Spain
FEATURES Location/Qualifiers

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RESULT 12
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DEFINITION   variant 2 (IREM1) mRNA, complete cds; alternatively spliced.
ACCESSION    AF375480
VERSION      AF375480.1  GI:30962590
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ORGANISM     Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 996)
AUTHORS      Alvarez-Errico,D., Kitzig,F., Sayos,J. and Lopez-Botet,M.
TITLE        Molecular and functional characterization of IREM-1, a novel
             inhibitory receptor expressed by myeloid cells
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 996)
AUTHORS      Alvarez-Errico,D., Kitzig,F., Sayos,J. and Lopez-Botet,M.
TITLE        Direct Submission
JOURNAL      Submitted (02-MAY-2001) Cexs/Immunology, Universitat Pompeu Fabra,
             Doctor Aiguader 80, Barcelona 08003, Spain
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             56..937
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             SPRKATTKLASAQVDQVEYVVTWASLPKEDISYASLTLLGAEDQEPYCNMHLSSHL
             PGRGPPEPTVSTISR"
ORIGIN
Query Match      49.0%; Score 880.6; DB 9; Length 996;
Best Local Similarity 98.8%; Pred. No. 9.1e-224;
Matches 880; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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DB 106 AGGCTACTCCATTGCCACTCAAATCACCGGTCCCAACACAGTGAATGGCTTGGAGCGGGG 165
QY 214 CTCCTTGACCGTGAGTGTGTTTACAGATCAGGCTGGAGACCTACTTGAAGTGGTGGT 273
DB 166 CTCCTTGACCGTGAGTGTGTTTACAGATCAGGCTGGAGACCTACTTGAAGTGGTGGT 225
QY 274 TCGAGGAGCTATTGGCGTGACTCGACATCCTTGTAAACACAGTGGGTGAGAGCAGGA 333
DB 226 TCGAGGAGCTATTGGCGTGACTCGACATCCTTGTAAACACAGTGGGTGAGAGCAGGA 285
QY 334 GGTGAAGAGGACCGGGTGTCCATCAAGGACAATCAGAAAAACCGACGTTCACTGTGAC 393
DB 286 GGTGAAGAGGACCGGGTGTCCATCAAGGACAATCAGAAAAACCGACGTTCACTGTGAC 345
QY 394 CATGAGAGCTCATGAAAACTGATGCTGACACTTCTGGTGTGAATGAGAAAACTGG 453
DB 346 CATGAGAGCTCATGAAAACTGATGCTGACACTTCTGGTGTGAATGAGAAAACTGG 405
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Best Local Similarity 84.1%; Pred. No. 1.3e-149;
Matches 749; Conservative 3; Mismatches 3; Indels 136; Gaps 1;
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D 106 AGGCTACTCCATTGTCATCAAAATCACCGGTCACACACAGTGAATGGCTTGGAGCGGGG 165
QY 214 CTCCTTGACCGTGAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGGTG 273
D 166 CTCCTTGACCGTGAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGGTG 225
QY 274 TCGAGGAGCTATTTGGCGTGACTGACAGATCCTTTGTTAAACACAGTGGGTGAGAGGAGGA 333
D 226 TCGAGGAGCTATTTGGCGTGACTGACAGATCCTTTGTTAAACACAGTGGGTGAGAGGAGGA 285
QY 334 GGTGAGAGGACCGGGTGTCCATCAGGAGCAATTCAGAAACCGGACGTTCACTGTGAC 393
D 286 GGTGAGAGGACCGGGTGTCCATCAGGAGCAATTCAGAAACCGGACGTTCACTGTGAC 345
QY 394 CATGAGGAGTCTCATGAAACTGATGCTGACACTTACTTGTGTGGAATTCAGAAACTGG 453
D 346 CATGAGGAGTCTCATGAAACTGATGCTGACACTTACTTGTGTGGAATTCAGAAACTGG 405
QY 454 AAATGACCTTGGGTTCAGTTCAGTGAACATTCAGTGAACCGGACGTTCACTGAGGAGGA 513
D 406 AAATGACCTTGGGTTCAGTTCAGTGAACATTCAGTGAACCGGACGTTCACTGAGGAGGA 465
QY 514 AACTAGAGCTCCCCAAGTCTGACCGGCGACACTTGCAGACAGGACAGCTCCTGAA 573
D 466 AACTAGAGCTCCCCAAGTCTGACCGGCGACACTTGCAGACAGGACAGCTCCTGAA 507
QY 574 GCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCGCGCTC 633
D 508 ----- 507
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D 508 -----CA 509
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D 510 GGTACTGAGCCCTGGAGGCGGACCTCTGCTATGACAGACTGACCTGAGTGGCGCGG 569
QY 754 AACTCTCCCGGGAAGGCTACCAAGAGCTTCTCTGCCAGGTTGAACAGTGAAGT 813
D 570 AACTCTCCCGGGAAGGCTACCAAGAGCTTCTCTGCCAGGTTGAACAGTGAAGT 629
QY 814 GGAATATGTACCAATGGCTTCTTTCGCGGAGGAGGACATTTCTATGATCTCTGACCTT 873
D 630 GGAATATGTACCAATGGCTTCTTTCGCGGAGGAGGACATTTCTATGATCTCTGACCTT 589
QY 874 GGGTGTGAGGATCAGGAACCGACTACTGCAACATGGGCGACCTCAGTAGCCACTCC 933
D 690 GGGTGTGAGGATCAGGAACCGACTACTGCAACATGGGCGACCTCAGTAGCCACTCC 749
QY 934 CGGAGGGGGCCCTGAGGAGCCCGGAAATACAGCACCATCAGAGGCGCTTAGCCTGCAT 993
D 750 CGGAGGGGGCCCTGAGGAGCCCGGAAATACAGCACCATCAGAGGCGCTTAGCCTGCAT 809
QY 994 CCAGGCTCCTTTTGGAGCCCGGAGGCTGTGAGCAGCACTCTCTGCTCATGAC 1044
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Db 810 CCAGGCTCCTTTTGGAGCCCGGAGGTGTGAGCACACTCTGCTCATGAC 860
RESULT 14
LOCUS BD058338 516 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted expressed sequence tags (SESTs).
ACCESSION BD058338
VERSION BD058338.1 GI:22603944
KEYWORDS JP 2001519666-A/193.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 516)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secreted expressed sequence tags (SESTs)
JOURNAL Patent: JP 2001519666-A 193 23-OCT-2001;
GENETICS INSTITUTE INC
COMMENT FN JP 2001519666-A/193
PD 23-OCT-2001
PF 10-APR-1998 JP 1998543068
PR 10-APR-1997 US 08/835913
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
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CC Topology: Linear;
FH Key Location/Qualifiers.
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ORIGIN
Query Match 25.9%; Score 465.4; DB 6; Length 516;
Best Local Similarity 97.2%; Pred. No. 7e-113;
Matches 484; Conservative 0; Mismatches 12; Indels 2; Gaps 1;
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D 16 GGCCTAANAGAAGATGCCCTGCTGATCAGTCTAACCTGCTCTTCTGCTCTCAGGC 75
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D 76 TACTCCATTGGCCTCAATACCGGTCACACAGTGAATGGCTGGAGCGGGGTCC 135
QY 218 TTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGTCGA 277
D 136 TTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGTCGA 195
QY 278 GGAGCTATTTGGCGTGAAGTCTGCAAGATCCTTGTAAAACAGTGGGTGAGAGAGGTG 337
D 196 GGAGCTATTTGGCGTGAAGTCTGCAAGATCCTTGTAAAACAGTGGGTGAGAGAGGTG 255
QY 338 AAGAGGACCGGGTGTCCATCAGGACAAATCAGAAAAACCGACGTTCACTGTGACCATG 397
D 256 AAGAGGACCGGGTGTCCATCAGGACAAATCAGAAAAACCGACGTTCACTGTGACCATG 315
QY 398 GAGGATCTCATGAAACTGATGCTGACACTTACTTGTGGAATTGAGAAACTGGAAT 457
D 316 GAGGATCTCATGAAACTGATGCTGACACTTACTTGTGGAATTGAGAAACTGGAAT 375
QY 458 GACCTTGGGTTCAGTTCAGTACCACTTACCCAGCAACGTCACCCAGAGAACT 517
D 376 GACCTTGGGTTCAGTTCAGTACCACTTACCCAGCAACGTCACCCAGAGAACT 435
QY 518 AGCAGCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGACAAAGCTCCTGAAGCTC 577
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 12:52:57 ; Search time 740 Seconds
(without alignments)

10310.492 Million cell updates/sec

Title: US-09-997-131-19

Perfect score: 1796

Sequence: 1 ggaaggaggaggttaagg.....aaaaaaaaaagcgcgccgc 1796

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373963 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
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9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1792.8	99.8	1796	3 AAC55198	AAC55198 Human sec
2	1741.6	97.0	1837	6 ABK3355	ABK3355 cDNA enco
3	1741.6	97.0	1837	7 ACA66860	ACA66860 cDNA enco
4	1741.6	97.0	1837	7 ACD68612	ACD68612 Novel hum
5	1741.6	97.0	1837	7 ACA68516	ACA68516 Novel hum
6	1741.6	97.0	1837	8 ABT44245	ABT44245 Human PRO
7	1741.6	97.0	1837	8 ABT44528	ABT44528 Human PRO
8	1741.6	97.0	1837	8 ACD82195	ACD82195 Human sec
9	1741.6	97.0	1837	8 ABT43901	ABT43901 Human mem
10	1741.6	97.0	1837	8 ADB83529	ADB83529 Novel hum
11	1741.6	97.0	1837	8 ADB80635	ADB80635 Novel hum
12	1741.6	97.0	1837	8 ADB73176	ADB73176 Novel hum
13	1741.6	97.0	1837	8 ADB78258	ADB78258 Novel hum
14	1741.6	97.0	1837	9 ADB84906	ADB84906 Human PRO
15	1741.6	97.0	1837	9 ADB78012	ADB78012 Novel hum
16	1741.6	97.0	1837	9 ADB87078	ADB87078 Human PRO
17	1741.6	97.0	1837	9 ADB84660	ADB84660 Human PRO
18	1741.6	97.0	1837	9 ADB83775	ADB83775 Novel hum
19	1741.6	97.0	1837	9 ADB72930	ADB72930 Novel hum
20	1741.6	97.0	1837	9 ADC36768	ADC36768 Human PRO
21	1741.6	97.0	1837	9 ADC21758	ADC21758 Human PRO
22	1741.6	97.0	1837	9 ADC49789	ADC49789 Novel hum
23	1741.6	97.0	1837	9 ADC48988	ADC48988 Novel hum

ALIGNMENTS

RESULT 1
AAC55198

ID AAC55198 standard; cDNA; 1796 BP.

AC AAC55198;

DT 16-JAN-2001 (first entry)

DE Human secreted protein gene 9 SEQ ID NO:19.

XX Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
XX Cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
XX Antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
XX Antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
XX agammaglobulinaemia; haematopoietic cell disorder; blood protein disorder;
XX autoimmune disease; hyperproliferative disease; Gaucher's disease;
XX cardiovascular disorder; congenital heart defect; pulmonary atresia;
XX arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
XX atherosclerosis; neurological disease; Alzheimer's disease;
XX Huntington's chorea; infectious disease; cat-scratch disease; SS.

XX Homo sapiens.

XX WO200047602-A1.

PD 17-AUG-2000.

PF 08-FEB-2000; 2000WO-US003062.

PR 10-FEB-1999; 99US-0119468P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;

XX Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;

XX WPI; 2000-543578/49.

XX P-PSDB; AAB32379.

XX New human nucleic acids encoding secreted proteins useful in the
XX treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
XX diseases), blood protein disorders and hyperproliferative diseases (e.g.
XX Gaucher's disease).

XX Claim 1; Page 396-397; 488pp; English.

XX

RESULT 2

ABK33555
ID ABK33555 standard; cDNA; 1837 BP.

XX ABK33555;
AC ABK33555;

XX 08-MAY-2002 (first entry)

DT
XX cDNA encoding human PRO protein, Seq ID No 39.

DE
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; Gene; ss.

XX Homo sapiens.

OS
XX WO200208288-A2.

PN
XX 31-JAN-2002.

XX
XX 29-JUN-2001; 2001WO-US021066.

XX
XX 20-JUL-2000; 2000US-0219556P.

XX
XX 25-JUL-2000; 2000US-0220585P.

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XX 25-JUL-2000; 2000US-0220605P.

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XX 25-JUL-2000; 2000US-0220607P.

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XX 25-JUL-2000; 2000US-0220624P.

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XX 25-JUL-2000; 2000US-0220638P.

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XX 26-JUL-2000; 2000US-0220893P.

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XX 28-JUL-2000; 2000WO-US020710.

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XX 01-AUG-2000; 2000US-0222425P.

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XX 23-AUG-2000; 2000WO-US023322.

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XX 24-AUG-2000; 2000WO-US023328.

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XX 10-NOV-2000; 2000WO-US030873.

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XX 28-NOV-2000; 2000US-0253646P.

XX
XX 01-DEC-2000; 2000WO-US032678.

XX
XX 20-DEC-2000; 2000US-00747259.

XX
XX 20-DEC-2000; 2000WO-US034356.

XX
XX 28-FEB-2001; 2001WO-US006520.

XX
XX 01-MAR-2001; 2001WO-US006566.

XX
XX 22-MAR-2001; 2001US-00816744.

XX
XX 10-MAY-2001; 2001US-00854208.

XX
XX 25-MAY-2001; 2001US-00854280.

XX
XX 25-MAY-2001; 2001WO-US017092.

PA (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Geritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX P-PSD8; AAU83611.

DR WPI; 2002-172001/22.

DR P-PSD8; AAU83611.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumors such
XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX or liver tumor.

XX Claim 2; Fig 39; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumors, especially lung
XX cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
XX liver tumor. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for

CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO
CC protein coding sequences of the invention

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SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 6; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTCTGTCGACGCTCCACTGAGGGAAC 91

DB 1 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTCTGTCGACGCTCCACTGAGGGAAC 60

QY 92 GGGGACCTGTCTGAAGAGAAATGCCCTCTGCTGACACTCTACCTGCTCTCTTCTGGCTC 151

DB 61 GGGGACCTGTCTGAAGAGAAATGCCCTCTGCTGACACTCTACCTGCTCTCTTCTGGCTC 120

QY 152 TCAGGCTACTCTCATTTGCCACTCAAAATCACCGTCCACACACAGTGAATGGCTTGGAGCGG 211

DB 121 TCAGGCTACTCTCATTTGCCACTCAAAATCACCGTCCACACACAGTGAATGGCTTGGAGCGG 180

QY 212 GGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271

DB 181 GGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240

QY 272 TGTGAGGAGCTATTGTCGCTGACTGCAAGATCCTTGTAAACACAGTGGTGGTGGTGGTGG 331

DB 241 TGTGAGGAGCTATTGTCGCTGACTGCAAGATCCTTGTAAACACAGTGGTGGTGGTGGTGG 300

QY 332 GAGGTGAAGAGGAGCCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACGTTCACTGTG 391

DB 301 GAGGTGAAGAGGAGCCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACGTTCACTGTG 360

QY 392 ACCATGGAGGATCTCATGAAATCTGATGCTGACACTTACTTGTGTTGGAATGGAGAACT 451

DB 361 ACCATGGAGGATCTCATGAAATCTGATGCTGACACTTACTTGTGTTGGAATGGAGAACT 420

QY 452 GGAATGACCTTGGGGTCAAGTTCAAGTGCACCAATGACCCAGCACAGTCAACCCAGAA 511

DB 421 GGAATGACCTTGGGGTCAAGTTCAAGTGCACCAATGACCCAGCACAGTCAACCCAGAA 480

QY 512 GAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGAACCACTTGGACCAAGGACAGCTCTG 571

DB 481 GAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGAACCAAGGACAGCTCTG 540

QY 572 AAGCTCAGTGTCTCTGCCCCCTCATCTTACCATATTTGTGTTTGTGGCGGCC 631

DB 541 AAGCTCAGTGTCTCTGCCCCCTCATCTTACCATATTTGTGTTTGTGGCGGCC 600

QY 632 TCACCTTGGCTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691

DB 601 TCACCTTGGCTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

QY 692 CAGTACTGAGCCCTTGGAGGCGACCTTGTGATGACAGCTGACCCCTGACAGTGGCC 751

DB 661 CAGTACTGAGCCCTTGGAGGCGACCTTGTGATGACAGCTGACCCCTGACAGTGGCC 720

QY 752 GGAACCTCCCGGAAAGGCTACAGAGCTTTCCTCTGCCAGGTTTACAGAGTGGAA 811

DB 721 GGAACCTCCCGGAAAGGCTACAGAGCTTTCCTCTGCCAGGTTTACAGAGTGGAA 780

QY 812 GTGGAATATGTCAACCATGGCTTCTTGGCAGAGGAGACATTTCTTATGCATCTCTGACC 871

DB 781 GTGGAATATGTCAACCATGGCTTCTTGGCAGAGGAGACATTTCTTATGCATCTCTGACC 840

QY 872 TTGGGTCTCAGGATCAGGAACGACCTACTGACATGGGCGCACTAGTACCACTT 931

DB 841 TTGGGTCTCAGGATCAGGAACGACCTACTGACATGGGCGCACTAGTACCACTT 900

QY 932 CCGGAGGGGCGCTGAGGAGCCAGCAATACAGCACCATCAGAGGCGCTTACCTGCA 991
 Db 901 CCGGAGGGGCGCTGAGAGGCCACCGAATACAGCACCATCAGAGGCGCTTACCTGCA 960
 QY 992 CTCAGGCTCCTTCTTGAGACCCAGGCTGTGAGCACACTCTCTGCTCATCGACGCTGTC 1051
 Db 961 CTCAGGCTCCTTCTTGAGACCCAGGCTGTGAGCACACTCTCTGCTCATCGACGCTGTC 1020
 QY 1052 CCCCTGCTCCCTCATCAGGACCCAGGAGCTGTGAGGCTCTCTGCTGATCAGCAGCA 1111
 Db 1021 CCCCTGCTCCCTCATCAGGACCCAGGAGCTGTGAGGCTCTCTGCTGATCAGCAGCA 1080
 QY 1112 TTGCCCTAGCTCTGGGTTGGCTTTGGGCGCCAGTCTCAGGGGCTTCTAGGAGTTGGG 1171
 Db 1081 TTGCCCTAGCTCTGGGTTGGCTTTGGGCGCCAGTCTCAGGGGCTTCTAGGAGTTGGG 1140
 QY 1172 TTTTCTAAAGTCCCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230
 Db 1141 TTTTCTAAAGTCCCTCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1200
 QY 1231 GGCCTTCAATGGGAATGATGAAGATGATAAATCAGAAATGTTATCATATCATGAAG 1290
 Db 1201 GGCCTTCAATGGGAATGATGAAGATGATAAATCAGAAATGTTATCATATCATGAAG 1260
 QY 1291 TACATTTATCATATGAATGAATCTTTATTTATGCTTACCAATGTTATGGGCTGAAT 1350
 Db 1261 TACATTTATCATATGAATGAATCTTTATTTATGCTTACCAATGTTATGGGCTGAAT 1320
 QY 1351 AATGGCCCCAAGATATCTGTGCTTAATCTCAGAACTGTGACTGTACCTTCTGTG 1410
 Db 1321 AATGGCCCCAAGATATCTGTGCTTAATCTCAGAACTGTGACTGTACCTTCTGTG 1380
 QY 1411 GCAGAAAGGACAGTGAGATGTATGTAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1470
 Db 1381 GCAGAAAGGACAGTGAGATGTATGTAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1440
 QY 1471 TGCTGATTCAGTGGGCGCCAAATATCACACAGGCTCTCATAGAAAGAGGCCAGAA 1530
 Db 1441 TGCTGATTCAGTGGGCGCCAAATATCACACAGGCTCTCATAGAAAGAGGCCAGAA 1500
 QY 1531 GGTCAAGAGTAGAGACAAAGTATGATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1590
 Db 1501 GGTCAAGAGTAGAGACAAAGTATGATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
 QY 1591 GCCATGATGCGGAGCTTCAGATGCCAGAAAGGAAAGATGATTCCTCTGCTGG 1650
 Db 1561 GCCATGATGCGGAGCTTCAGATGCCAGAAAGGAAAGATGATTCCTCTGCTGG 1620
 QY 1651 AGCTCCAAAGAAACAGGCTCCACAGCTTGTGCTGAGCCCTTGAATGAACTGATCTT 1710
 Db 1621 AGCTCCAAAGAAACAGGCTCCACAGCTTGTGCTGAGCCCTTGAATGAACTGATCTT 1680
 QY 1711 GAGCTCTGCTCCAGAAATGAGGAGAAATAATTGTTGTTTAAATGAAAGAAAA 1770
 Db 1681 GAGCTCTGCTCCAGAAATGAGGAGAAATAATTGTTGTTTAAATGAAAGAAAA 1740
 QY 1771 AAAAAAAAAAAAAA 1786
 Db 1741 AAAAAAAAAAAAAA 1756

RESULT 3

ACA66860

ID ACA66860 standard; cDNA; 1837 BP.

XX ACA66860;

AC ACA66860;

DT 23-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #20.

XX Human; PRO polypeptide; secreted and transmembrane protein;

KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
 gene; ss.

Homo sapiens.

US2003036635-A1.

20-FEB-2003.

28-AUG-2002; 2002US-00230163.

25-JUL-2000; 2000US-0220638P.

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US021066.

09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

WPI: 2003-342045/32.

P-PSDB; AB080758.

One hundred and twenty two nucleic acids encoding PRO polypeptides,
 useful for the manufacture of a medicament for diagnosing or treating
 tumor.

Claim 2; Fig 39; 314pp; English.

The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The PRO
 polypeptides are secreted and transmembrane proteins. The PRO
 polypeptides and polynucleotides are useful for preparing a medicament
 useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
 useful in diagnostic assays for PRO, by detecting its expression in
 specific cells, tissues or serum, and for affinity purification of PRO
 from recombinant cell culture or natural sources. ACA66841-ACA66962
 represent cDNA sequences encoding the human PRO polypeptides of the
 invention. Note: The sequence data for this patent was obtained in
 electronic format directly from the USPTO web site at
 seqdata.uspto.gov/psipdbIDentry.html

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 7; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGGAGTCTGTAGTTGTTCCTGCTGCCAGGCTCCACTGAGGGGAAC 91

Db 1 ACCAGCAGAGGCTGGGAGTCTGTAGTTGTTCCTGCTGCCAGGCTCCACTGAGGGGAAC 60

QY 92 GGGGACCTGTCTGAAGAGAAAGATGCCCTGTGACACTCTACCTGCTCCTCTTCTGGCTC 151

Db 61 GGGGACCTGTCTGAAGAGAAAGATGCCCTGTGACACTCTACCTGCTCCTCTTCTGGCTC 120

QY 152 TCAGGCTACTCCATTGCCACTCAAAATCACGGTCCAAACAGATGGAATGCTTGAGCGG 211

Db 121 TCAGGCTACTCCATTGCCACTCAAAATCACGGTCCAAACAGATGGAATGCTTGAGCGG 180

QY 212 GGCTCCTTGACCGTGCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 271

Db 181 GGCTCCTTGACCGTGCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 240

QY 272 TGTGAGAGCTATTGGCGTGACTGCAAGATCCTTTAAACCACTGGGTGAGAGCAG 331

Db 241 TGTGAGAGCTATTGGCGTGACTGCAAGATCCTTTAAACCACTGGGTGAGAGCAG 300

QY 332 GAGGTGAAGGGGACCGGCTGCCATCAAGGACAAATCAGAAACCCGACGTTCACTGTG 391

Db 301 GAGGTGAAGGGGACCGGCTGCCATCAAGGACAAATCAGAAACCCGACGTTCACTGTG 360

CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 7; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY	32	ACCAGCAGAGGCTGGGAGTCTGTAGTTTCTGCTGCGCAGGCTCCACTGAGGGGAAC	91
DB	1	ACCAGCAGAGGCTGGGAGTCTGTAGTTTCTGCTGCGCAGGCTCCACTGAGGGGAAC	60
QY	92	GGGACCTGTCTGAAGAAAGATGCCCCCTGTGTGACACTTCTACCTGCTCCTCTTGGCTC	151
DB	61	GGGACCTGTCTGAAGAAAGATGCCCCCTGTGTGACACTTCTACCTGCTCCTCTTGGCTC	120
QY	152	TCAGGCTACTGATTCGACCTCAATACACCGGTGCACACAGTGAATGGCTGGAGCGG	211
DB	121	TCAGGCTACTGATTCGACCTCAATACACCGGTGCACACAGTGAATGGCTGGAGCGG	180
QY	212	GGCTCTTACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTACTTGAAGTGTGG	271
DB	181	GGCTCTTACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTACTTGAAGTGTGG	240
QY	272	TGTGAGGAGTATTTGGCGTGAATGCAAGATCTTGTGTTAAAAACAGTGGGTGAGACAG	331
DB	241	TGTGAGGAGTATTTGGCGTGAATGCAAGATCTTGTGTTAAAAACAGTGGGTGAGACAG	300
QY	332	GAGGTGAAGAGGACCGGGTGCATCAAGACCAATCAGAAAAACCGACGTTCACTGTG	391
DB	301	GAGGTGAAGAGGACCGGGTGCATCAAGACCAATCAGAAAAACCGACGTTCACTGTG	360
QY	392	ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGAAATTGAGAAAACT	451
DB	361	ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGAAATTGAGAAAACT	420
QY	452	GGAATGACCTTGGGTCACAGTTCAGTGAACCTTGCACCGACCAATCAGGACCAAGTCA	511
DB	421	GGAATGACCTTGGGTCACAGTTCAGTGAACCTTGCACCGACCAATCAGGACCAAGTCA	480
QY	512	GAAATAGCAGCTCCCAACTCTGACCGGCCCACTTGGACAAACAGGCAACAGCTCCTG	571
DB	481	GAAATAGCAGCTCCCAACTCTGACCGGCCCACTTGGACAAACAGGCAACAGCTCCTG	540
QY	572	AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCGCC	631
DB	541	AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCGCC	600
QY	632	TCACCTCTTGGCTTGAGGATGATGAAGTACCAGACAGAAAGCAGCGGGATGTCCCCAGAG	691
DB	601	TCACCTCTTGGCTTGAGGATGATGAAGTACCAGACAGAAAGCAGCGGGATGTCCCCAGAG	660
QY	692	CAGGTACTGACGCCCTGGAGGGGCACTCTGCTATGACGACCTGACCCCTGACGCTGCC	751

DB	661	CAGGTACTGACGCCCTGGAGGGGCACTTGTCTATGACGACCTGACCTGACGCTGCC	720
QY	752	GGAACCTCCCGCGAAAGGCTACCAAGAGCTTTCTGTGCCAGGTTGACAGGTGAA	811
DB	721	GGAACCTCCCGCGCGAAAGGCTACCAAGAGCTTTCTGTGCCAGGTTGACAGGTGAA	780
QY	812	GTGGAATATGTCACCATGCTTCTTCCGAGAGGAGACATTTCTATGCACTCTGACC	871
DB	781	GTGGAATATGTCACCATGCTTCTTCCGAGAGGAGACATTTCTATGCACTCTGACC	840
QY	872	TTGGGTGCTGAGGATCAGGAAACCGACCTACTGTCAAATGGGCGCACTCAGTAGCCACT	931
DB	841	TTGGGTGCTGAGGATCAGGAAACCGACCTACTGTCAAATGGGCGCACTCAGTAGCCACT	900
QY	932	CCCGCAGGGGCGCTGAGGAGCCGAGGATACAGACCATCAGCAGGCTTAGGCTGCA	991
DB	901	CCCGCAGGGGCGCTGAGGAGCCGAGGATACAGACCATCAGCAGGCTTAGGCTGCA	960
QY	992	CTCCAGGCTCTTCTTGGACCCCGAGGCTGTGAGACACTCTCTGCTCATGACCGTCTGC	1051
DB	961	CTCCAGGCTCTTCTTGGACCCCGAGGCTGTGAGACACTCTCTGCTCATGACCGTCTGC	1020
QY	1052	CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTGCTCTGCTGATCAGCAGCA	1111
DB	1021	CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTGCTCTGCTGATCAGCAGCA	1080
QY	1112	TTGCCCCCTAGCTCTGGTTGGGCTTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG	1171
DB	1081	TTGCCCCCTAGCTCTGGTTGGGCTTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG	1140
QY	1172	TTTTCTAAACGTCCTCTCTCT-CTACATAGTTGAGGAGGGGGCTTAGGGATATGCTCTGG	1230
DB	1141	TTTTCTAAACGTCCTCTCTCTCTACATAGTTGAGGAGGGGGCTTAGGGATATGCTCTGG	1200
QY	1231	GGCTTTCATGGCAATGATGAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1290
DB	1201	GGCTTTCATGGCAATGATGAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1260
QY	1291	TACCATTTATCATTAATACTAACTTTATTTATGCTTACACATGTTATGGGCTGAAT	1350
DB	1261	TACCATTTATCATTAATACTAACTTTATTTATGCTTACACATGTTATGGGCTGAAT	1320
QY	1351	AATGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTACCTTCTGTG	1410
DB	1321	AATGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTACCTTCTGTG	1380
QY	1411	GCAGAAAGGACAGTGCAGATGATGTAAGTTAAAGCTTTTGAATAGAGAGGTTATTTCT	1470
DB	1381	GCAGAAAGGACAGTGCAGATGATGTAAGTTAAAGCTTTTGAATAGAGAGGTTATTTCT	1440
QY	1471	TGCTGATTCAGTGGGCGCAAAATATACCAACAGGGTCTCTATAGAAAGAGGCGCAAA	1530
DB	1441	TGCTGATTCAGTGGGCGCAAAATATACCAACAGGGTCTCTATAGAAAGAGGCGCAAA	1500
QY	1531	GGTCAAGAGGTAGAGACAAAGTGTATGAAAGTGGACGCTGGGTGTGACGTCAGCAGGG	1590
DB	1501	GGTCAAGAGGTAGAGACAAAGTGTATGAAAGTGGACGCTGGGTGTGACGTCAGCAGGG	1560
QY	1591	GCCATGAATGCCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCTGCTGG	1650
DB	1561	GCCATGAATGCCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCTGCTGG	1620
QY	1651	AGCTCCCAAGAAAGAGCCCTGCCCTGCTGACCTTGCATTTGAGCCCATTTGAACTGATCTT	1710
DB	1621	AGCTCCCAAGAAAGAGCCCTGCCCTGCTGACCTTGCATTTGAGCCCATTTGAACTGATCTT	1680
QY	1711	GAGCTCTGGCTCCAGAAATTGACAGAGATAAATTTGTTGTTTAAATGAAAAAAA	1770
DB	1681	GAGCTCTGGCTCCAGAAATTGACAGAGATAAATTTGTTGTTTAAATGAAAAAAA	1740
QY	1771	AAAAAAAAAAAAAAAAAAAA 1786	

Qy	692	CAGGTACTGCAGCCCTGGAGGGCGACCTCTGCTATGCGAGCCTGACCCCTGCAGTGGCC	751
Db	661	CAGGTACTGCAGCCCTGGAGGGCGACCTCTGCTATGCGAGCCTGCAGTGGCC	720
Qy	752	GGAACTCCCGCGAAAGGCTACCA GGAAGCTTTCCTCTGCCAGGTTGACGAGTGGAA	811
Db	721	GGAACTCCCGCGAAAGGCTACCA GGAAGCTTTCCTCTGCCAGGTTGACGAGTGGAA	780
Qy	812	GTGGAATATGTCACCATGGCTTCCTTTCGCCAAGGAGGACATTTCTCTATGCATCTCTGACC	871
Db	781	GTGGAATATGTCACCATGGCTTCCTTTCGCCAAGGAGGACATTTCTCTATGCATCTCTGACC	840
Qy	872	TTGGGTGTCAGGATCAGGAACCGACTACTGGAACATGGGGCCAMCTCAGTAGCCMCTY	931
Db	841	TTGGGTGTCAGGATCAGGAACCGACTACTGGAACATGGGGCCAMCTCAGTAGCCMCTC	900
Qy	932	CCGGCAGGGGCCCTGAGGAGCCACGGAAATACAGACCATCAGCAGGCTTAGCCTGCA	991
Db	901	CCGGCAGGGGCCCTGAGGAGCCACGGAAATACAGACCATCAGCAGGCTTAGCCTGCA	960
Qy	992	CTCAGGCTCCTTTCTGGACCCCGAGGCTGTGACACACTCTCCCTCATCGACCGCTCG	1051
Db	961	CTCAGGCTCCTTTCTGGACCCCGAGGCTGTGACACACTCTCCCTCATCGACCGCTCG	1020
Qy	1052	CCCTGCTCCCTCATCAGAACCAACCCGGGACTGGTGCCTCTGCCTGATCAGCCAGCA	1111
Db	1021	CCCTGCTCCCTCATCAGAACCAACCCGGGACTGGTGCCTCTGCCTGATCAGCCAGCA	1080
Qy	1112	TTGGCCCTAGCTCTGGGTTCGGCTTGGGGCCAAAGTCTCAGGGGCTCTTAGAGAGTTGGGG	1171
Db	1081	TTGGCCCTAGCTCTGGGTTCGGCTTGGGGCCAAAGTCTCAGGGGCTCTTAGAGAGTTGGGG	1140
Qy	1172	TTTTCTAAACGTCCCTCCCTCTCTCATATAGTTGAGAGGGGGCTAGGAGATATGCTCTGG	1230
Db	1141	TTTTCTAAACGTCCCTCCCTCTCTCATATAGTTGAGAGGGGGCTAGGAGATATGCTCTGG	1200
Qy	1231	GGCTTTCATGGGAATGATGAAGATGAATAGAGAAAATGTTATCATATTATCATCAAG	1290
Db	1201	GGCTTTCATGGGAATGATGAAGATGAATAGAGAAAATGTTATCATATTATCATCAAG	1260
Qy	1291	TACCATTTATCATATACAAATGAACCTTTATTTATGCTTACCACATGTTATGGCTGAAT	1350
Db	1261	TACCATTTATCATATACAAATGAACCTTTATTTATGCTTACCACATGTTATGGCTGAAT	1320
Qy	1351	AATGGCCCCCAAGATATCTGTGTCCTAAATCTCTCAGAACTGTGACTGTTTACCTTCTGG	1410
Db	1321	AATGGCCCCCAAGATATCTGTGTCCTAAATCTCTCAGAACTGTGACTGTTTACCTTCTGG	1380
Qy	1411	GCAGAAAGGGACGTGCAGATGTATGAAGTTAAGGACTTTTGATATAGAGAGTTATCT	1470
Db	1381	GCAGAAAGGGACGTGCAGATGTATGAAGTTAAGGACTTTTGATATAGAGAGTTATCT	1440
Qy	1471	TGCTGATTCAGGTGGGCCCAAAATATACCAACAAGGTCCTCTATAAGAAAGAGCCAGAA	1530
Db	1441	TGCTGATTCAGGTGGGCCCAAAATATACCAACAAGGTCCTCTATAAGAAAGAGCCAGAA	1500
Qy	1531	GGTCAAGAGGTAGAGCAAGTATCATATGGAAGTGGACGTGGGTGAGCGTGGAGAGGG	1590
Db	1501	GGTCAAGAGGTAGAGCAAGTATCATATGGAAGTGGACGTGGGTGAGCGTGGAGAGGG	1560
Qy	1591	GCCATGAATGCGCAGGCTTCAGATGCGCAGAAAGGAAGATGGATTCCTCCCTGCCTGG	1650
Db	1561	GCCATGAATGCGCAGGCTTCAGATGCGCAGAAAGGAAGATGGATTCCTCCCTGCCTGG	1620
Qy	1651	AGCCTCCAAAAGAAACAGCCCTGCCTCAGCGCTTGACCTTGAGCCCATTTGAACTGATCTT	1710
Db	1621	AGCCTCCAAAAGAAACAGCCCTGCCTCAGCGCTTGACCTTGAGCCCATTTGAACTGATCTT	1680
Qy	1711	GAGCTCCTGGCCTCCAGAAATTCGAGGAGAAATAAATTTGTGTGTTTATGAAAAAAA	1770
Db	1681	GAGCTCCTGGCCTCCAGAAATTCGAGGAGAAATAAATTTGTGTGTTTATGAAAAAAA	1740

PT	chromosome markers, or in generating probes.	
XX	Claim 2; Fig 39; 315pp; English.	
XX	The invention relates to an isolated nucleic acid encoding a PRO	
CC	polypeptide. Nucleic acids that encode PRO can be used to generate either	
CC	transgenic animals or knock-out animals useful in developing and	
CC	screening of therapeutically useful reagents. The nucleic acids may also	
CC	be used in gene therapy for replacing defective gene, in chromosome	
CC	identification, as chromosome markers, or in generating probes to isolate	
CC	full length PRO cDNA. The PRO polypeptides are useful for chondrocyte	
CC	stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation	
CC	and for detecting the presence of tumour in an mammal. The PRO	
CC	polypeptides are useful as molecular markers for protein electrophoresis	
CC	and the isolated nucleic acids may be used for recombinantly expressing	
CC	those markers. The PRO polypeptides and nucleic acids may also be used in	
CC	tissue typing. Anti-PRO antibodies are useful in diagnostic assays for	
CC	PRO and in affinity purification of PRO from recombinant cell culture or	
CC	natural sources. The present sequence represents cDNA encoding a human	
CC	secreted/transmembrane PRO polypeptide	
XX	Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;	
SQ		
	Query Match 97.0%; Score 1741.6; DB 8; Length 1837;	
	Best Local Similarity 99.6%; Pred. No. 0;	
	Matches 1749; Conservative. 6; Mismatches 0; Indels 1; Gaps 1;	
QY	32 ACCAGCAGAGGCTGGGAGTCTGTAGTTTCTGCTGCTCCAGGCTCCACTGAGGGGAAC 91	
DB	1 ACCAGCAGAGGCTGGGAGTCTGTAGTTTCTGCTGCTCCAGGCTCCACTGAGGGGAAC 60	
QY	92 GGGGACCTGTCTGAAGAGAGATGCCCTCTGTGACACTTACCTGTCTCTCTCTCTGCTC 151	
DB	61 GGGGACCTGTCTGAAGAGAGATGCCCTCTGTGACACTTACCTGTCTCTCTCTCTGCTC 120	
QY	152 TCAGGCTACTCCATTGGCCACTCAATCACCGGTCCAAACACAGTGAATGCTTGGAGCG 211	
DB	121 TCAGGCTACTCCATTGGCCACTCAATCACCGGTCCAAACACAGTGAATGCTTGGAGCG 180	
QY	212 GGCTCCTTGACCGTGACGTGTTTACAGATCAGGCTGGGAGACTTACTTTGAATGTTGG 271	
DB	181 GGCTCCTTGACCGTGACGTGTTTACAGATCAGGCTGGGAGACTTACTTTGAATGTTGG 240	
QY	272 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTTTAAACACAGTGGGTGAGAGCAG 331	
DB	241 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTTTAAACACAGTGGGTGAGAGCAG 300	
QY	332 GAGGTGAAGAGGACCGGGTGTCCATCAAGACATCAGAAACCCGACGTTCACTGTG 391	
DB	301 GAGGTGAAGAGGACCGGGTGTCCATCAAGACATCAGAAACCCGACGTTCACTGTG 360	
QY	392 ACCATGGAGGATCTCATGAAACCTGATGCTGACACTTACTGGTGTGGAATTGAGAAACT 451	
DB	361 ACCATGGAGGATCTCATGAAACCTGATGCTGACACTTACTGGTGTGGAATTGAGAAACT 420	
QY	452 GGAAATGACCTTTGGGGTCAAGTTCAGTGAACATTCAGACCCAGACACAGTCAACCAAGAA 511	
DB	421 GGAAATGACCTTTGGGGTCAAGTTCAGTGAACATTCAGACCCAGACACAGTCAACCAAGAA 480	
QY	512 GAACCTAGCAGTCCCAACCTGACCGGCCACCACTTGGCAACAGGCAACAGTCTCTG 571	
DB	481 GAACCTAGCAGTCCCAACCTGACCGGCCACCACTTGGCAACAGGCAACAGTCTCTG 540	
QY	572 AAGCTCAGTGTCTCTCTGCTCCCTCATCTTCACCATATTTKTYGTGTTTGGTGGCGGCC 631	
DB	541 AAGCTCAGTGTCTCTCTGCTCCCTCATCTTCACCATATTTGCTGCTCTTTTGGTGGCGGCC 600	
QY	632 TCACCTTTGGCTTGGAGATGATGAATACAGAGAGAGAGCGGGATGTCCCCAGAG 691	
DB	601 TCACCTTTGGCTTGGAGATGATGAATACAGAGAGAGAGCGGGATGTCCCCAGAG 660	
QY	692 CAGGTACTGACGCGCTGGAGGCGACCTCTGCTATGACAGACTGACCTCAGCTGCGCC 751	

661	CAGGTACTGACGCCCCCTGGAGGGGACCTCTGCTATGACAGACCTGACCCCTGACGTGGCC 720	DB
752	GGAACTCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCTCCCAAGTTGACCAAGTGA 811	QY
721	GGAACTCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCTCCCAAGTTGACCAAGTGA 780	DB
812	GTGGAATATGTACCATGGCTTCTTTCGGAAGGAGGACATTTCTCTATGCACTCTGACC 871	QY
791	GTGGAATATGTACCATGGCTTCTTTCGGAAGGAGGACATTTCTCTATGCACTCTGACC 840	DB
872	TGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCCACCTCAGTAGCCAMCTY 931	QY
841	TGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCCACCTCAGTAGCCAMCTY 900	DB
932	CCCGCAGGGGCTCTGAGAGCCCAACGGAATACAGCACCATCAGCAGGCTTAGCCTGCA 991	QY
901	CCCGCAGGGGCTCTGAGAGCCCAACGGAATACAGCACCATCAGCAGGCTTAGCCTGCA 960	DB
992	CTCCAGGCTCTCTTCTGAGCCCGCAGGCTGTGAGCACACTCTCTGCTCATGCACTGTGC 1051	QY
961	CTCCAGGCTCTCTTCTGAGCCCGCAGGCTGTGAGCACACTCTCTGCTCATGCACTGTGC 1020	DB
1052	CCCTGCTCCCTCATCAGGACCAACCGGGGACTGGTGCCTCTGCTGATCAGCCAGCA 1111	QY
1021	CCCTGCTCCCTCATCAGGACCAACCGGGGACTGGTGCCTCTGCTGATCAGCCAGCA 1080	DB
1112	TTGCCCTAGCTCTGGGTGGGCTTGGGCTCAAGTCTCAGGGGGCTTCTAGAGTGGGG 1171	QY
1081	TTGCCCTAGCTCTGGGTGGGCTTGGGCTCAAGTCTCAGGGGGCTTCTAGAGTGGGG 1140	DB
1172	TTTTCTAAACGTCCTCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230	QY
1141	TTTTCTAAACGTCCT 1200	DB
1231	GGCTTCTAGGGAATGATGAGATGATGAGAAAAATGTTATCATTTATTCATGAG 1290	QY
1201	GGCTTCTAGGGAATGATGAGATGATGAGAAAAATGTTATCATTTATTCATGAG 1260	DB
1291	TACCATTTATTAATACAAATGAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAT 1350	QY
1261	TACCATTTATTAATACAAATGAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAT 1320	DB
1351	AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1410	QY
1321	AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1380	DB
1411	GCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTTCAGATAGAGAGTTATCT 1470	QY
1381	GCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTTCAGATAGAGAGTTATCT 1440	DB
1471	TGCTGATTCAGGTGGGCCCCCAAAATATCACCACAGGCTCTCTATGAAGAGGCGCAGAA 1530	QY
1441	TGCTGATTCAGGTGGGCCCCCAAAATATCACCACAGGCTCTCTATGAAGAGGCGCAGAA 1500	DB
1531	GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTTAAGGAGTGGAGTGGGTGTGACGAGCGG 1590	QY
1501	GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTTAAGGAGTGGAGTGGGTGTGACGAGCGG 1560	DB
1591	GCCATGATTCGCGCAGCTTCAGATGCCAGAAAGGGAAGGATGGATTCCTCCCTGCTGG 1650	QY
1561	GCCATGATTCGCGCAGCTTCAGATGCCAGAAAGGGAAGGATGGATTCCTCCCTGCTGG 1620	DB
1651	AGCTCCAAAAGAAACACGCTCCCGCTTGTGCTTGTGAGCCCATTTGAAACTGATCTT 1710	QY
1621	AGCTCCAAAAGAAACACGCTCCCGCTTGTGCTTGTGAGCCCATTTGAAACTGATCTT 1680	DB
1711	GAGCTCTCTGCTCCAGAAATTCAGAGAAATAAATTTGTTGTTTATGAAAAAAA 1770	QY
1681	GAGCTCTCTGCTCCAGAAATTCAGAGAAATAAATTTGTTGTTTATGAAAAAAA 1740	DB
1771	AAAAAAAAAAAAAAAA 1786	QY
1741	AAAAAAAAAAAAAAAA 1756	DB

1112 TTGCCCCAGTCTGGGTTGGGCTTGGGCCCCAAGTCTCAGGGGGCTTCTAGAGTTGGG 1171
1081 TTGCCCCAGTCTGGGTTGGGCTTGGGCCCCAAGTCTCAGGGGGCTTCTAGAGTTGGG 1140
1172 TTTTCTAAAGTCCCTCTCTCTCTACATAGTTAGAGGGGGCTAGGATATGCTCTGG 1230
1141 TTTTCTAAAGTCCCTCTCTCTCTACATAGTTAGAGGGGGCTAGGATATGCTCTGG 1200
1231 GCGTTTCATGGGAATGATGAAGATGATGAATGAGAAAAATGTTATCATTTATTCATGAAG 1290
1201 GCGTTTCATGGGAATGATGAAGATGATGAATGAGAAAAATGTTATCATTTATTCATGAAG 1260
1291 TACATATATCAATCAATGAACCTTTATTTATTCGCTACACATGTTATGGGCTGAAT 1350
1261 TACCATATCAATCAATGAACCTTTATTTATTCGCTACACATGTTATGGGCTGAAT 1320
1351 AATGGCCCCCAAGATATGTTGTTCTTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
1321 AATGGCCCCCAAGATATGTTGTTCTTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1380
1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGCACTTTGAGATGAGAGTTATTCCT 1470
1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGCACTTTGAGATGAGAGTTATTCCT 1440
1471 TGCTGATTCAGTGGGCCCCCAATATCACCACAGGGTCTCTATAGAAAGAGGCCAGAA 1530
1441 TGCTGATTCAGTGGGCCCCCAATATCACCACAGGGTCTCTATAGAAAGAGGCCAGAA 1500
1531 GGTCAAGAGGTGAGACAAAGTATGATGAAGTGAAGTGGTGTGAGCTGAGCAGGG 1590
1501 GGTCAAGAGGTGAGACAAAGTATGATGAAGTGAAGTGGTGTGAGCTGAGCAGGG 1560
1591 GCAATGATCCGAGGCTTCAGATGTCAGAAAGGGAAGGAATGATTCCTCTGCTGG 1650
1561 GCAATGATCCGAGGCTTCAGATGTCAGAAAGGGAAGGAATGATTCCTCTGCTGG 1620
1651 AGCTCTCAAGAAACAGGCTTCCACACAGGCTTGAATGAGCCCAATGAACTGATCTT 1710
1621 AGCTCTCAAGAAACAGGCTTCCACACAGGCTTGAATGAGCCCAATGAACTGATCTT 1680
1711 GAGCTCTGCGCTCCAGAAATGAGGAGAAATAATTTGTTGTTTATGAAAAAAA 1770
1681 GAGCTCTGCGCTCCAGAAATGAGGAGAAATAATTTGTTGTTTATGAAAAAAA 1740
1771 AAAAAA 1786
1741 AAAAAA 1756

RESULT 10
ADB83529
ID ADB83529 standard; cDNA; 1837 BP.
AC ADB83529;
OS
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10111 cDNA.
XX human; secreted and transmembrane protein; PRO; gene; ss; cytostatic;
KW vulnary; antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX Homo sapiens.
OS
XX US2003073814-A1.
PN

XX 17-APR-2003.
PD 12-AUG-2002; 2002US-00218849.
XX
PF 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PV;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WJ;
PI WPI: 2003-644806/61.
XX P-PSDB; ADB83530.
DR
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX
PS Claim 2; Fig 39; 315pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO1071, PRO1411, PRO1309,
CC PRO1425, PRO1134, PRO826, PRO1005, PRO809, PRO1274, PRO1412,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1309,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1828, PRO1801, PRO1801, PRO1333, PRO3543, PRO3444, PRO4322,
CC PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This sequence encodes a human secreted and transmembrane
CC PRO polypeptide.
XX
SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
Best local similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
32 ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTGTCGCGAGGCTCCACTGAGGGGAAAC 91
1 ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTGTCGCGAGGCTCCACTGAGGGGAAAC 60
92 GGGGACCTCTTGAAGAGAGAGATGCCCTGCTGACACTTACTCTCTCTCTCTCTCTCTCT 151
61 GGGGACCTCTTGAAGAGAGAGATGCCCTGCTGACACTTACTCTCTCTCTCTCTCTCTCT 120

QY 152 TCAGGCTACTCCATTGCGCACTCAAAATCAACCGCTCCAAACAACAGTGAATGGCTTGAGCGG 211
 Db 121 TCAGGCTACTCCATTGCGCACTCAAAATCAACCGCTCCAAACAACAGTGAATGGCTTGAGCGG 180
 QY 212 GGCTCTTGACCGCTGACGCTGCTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 271
 Db 181 GGCTCTTGACCGCTGACGCTGCTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 240
 QY 272 TCTCAGAGAGCTATTGTCGCTGACCTGCAAGATCCTCTTTAAACCAAGTGGCTCAGAGAG 331
 Db 241 TCTCAGAGAGCTATTGTCGCTGACCTGCAAGATCCTCTTTAAACCAAGTGGCTCAGAGAG 300
 QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACCGTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACCGTTCACTGTG 360
 QY 392 ACCATGGAGGATCTCATGAATACTGATGCTGACACTTACTGCTGGTGTGGAATTTAGAAAACT 451
 Db 361 ACCATGGAGGATCTCATGAATACTGATGCTGACACTTACTGCTGGTGTGGAATTTAGAAAACT 420
 QY 452 GGAAATGACCTTGGGGTCAACAGTTCAAGTGCACCTTGAACCCAGCACAGTCAACCAAGAA 511
 Db 421 GGAAATGACCTTGGGGTCAACAGTTCAAGTGCACCTTGAACCCAGCACAGTCAACCAAGAA 480
 QY 512 GAACTAGAGCTCCCCAACTCTGACCGGCAACCACTTGGGCAACAGGCAACAGCTCTG 571
 Db 481 GAACTAGAGCTCCCCAACTCTGACCGGCAACCACTTGGGCAACAGGCAACAGCTCTG 540
 QY 572 AAGCTCAGTGTCTCTCCCTCATCTTCAACATATKTYGTCTTTGGTGGCCGCC 631
 Db 541 AAGCTCAGTGTCTCTCCCTCATCTTCAACATATKTYGTCTTTGGTGGCCGCC 600
 QY 632 TCACCTTTGGCTTGAGGATGATGAAGTACCAGCAGAAAGCAGCCGGATGTCCCCAGAG 691
 Db 601 TCACCTTTGGCTTGAGGATGATGAAGTACCAGCAGAAAGCAGCCGGATGTCCCCAGAG 660
 QY 692 CAGGTACTGACGCCCTGGAGGGGACCTCTGCTATGACAGACCTGACCCCTGCAGCTGGCC 751
 Db 661 CAGGTACTGACGCCCTGGAGGGGACCTCTGCTATGACAGACCTGACCCCTGCAGCTGGCC 720
 QY 752 GGAACCTCCCGCGAAAGGCTACACGAAAGCTTTCTCTGCCCCAGGTTGACCAAGTGGAA 811
 Db 721 GGAACCTCCCGCGAAAGGCTACACGAAAGCTTTCTCTGCCCCAGGTTGACCAAGTGGAA 780
 QY 812 GTGGAATATGTCACGATGGCTTCTTCCGAGAGGAGACATTTCCCTATGATCTCTGACC 871
 Db 781 GTGGAATATGTCACGATGGCTTCTTCCGAGAGGAGACATTTCCCTATGATCTCTGACC 840
 QY 872 TTGGTGTCTGAGGATCAGGAACCGACCTACTCTGCAACATGGGCCAMCTCAGTAGCCAMCTY 931
 Db 841 TTGGTGTCTGAGGATCAGGAACCGACCTACTCTGCAACATGGGCCAMCTCAGTAGCCAMCTY 900
 QY 932 CCCGCGAGGGCCCTGAGGAGCCCAACGGAATACAGCAACATCAGAGGCTTACGCTGCA 991
 Db 901 CCCGCGAGGGCCCTGAGGAGCCCAACGGAATACAGCAACATCAGAGGCTTACGCTGCA 960
 QY 992 CTCAGAGCTCTCTTCTGAGCCCGGAGGCTGTGAGCACAACCTCTGCTCATCGACCGCTGC 1051
 Db 961 CTCAGAGCTCTCTTCTGAGCCCGGAGGCTGTGAGCACAACCTCTGCTCATCGACCGCTGC 1020
 QY 1052 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1111
 Db 1021 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1080
 QY 1112 TTGGCCCTAGCTCTGGTGTGGCTTGGGCCCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1171
 Db 1081 TTGGCCCTAGCTCTGGTGTGGCTTGGGCCCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1140
 QY 1172 TTTTCTAAACGTCCTCCCTCTCT-CTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG 1230
 Db 1141 TTTTCTAAACGTCCTCCCTCTCTCTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG 1200
 QY 1231 GGCTTTTCATGGGAATGATGAGATGATTAATGAGAAAAATGTTATCATATTATCATGAAG 1290

Db 1201 GGCTTTTCATGGGAATGATGAGATGATTAATGAGAAAAATGTTATCATTTATTCATGAAG 1260
 QY 1291 TACCATTATCATTAATCAATGAACCTTTATTTATTTGCTTACCACATGTTTATGGGTGAAT 1350
 Db 1261 TACCATTATCATTAATCAATGAACCTTTATTTATTTGCTTACCACATGTTTATGGGTGAAT 1320
 QY 1351 AATGGCCCCCAAGATATCTGTCTCTTAATCTCTGAACTCTGAACTCTGAACTCTGAACTCTG 1410
 Db 1321 AATGGCCCCCAAGATATCTGTCTCTTAATCTCTGAACTCTGAACTCTGAACTCTGAACTCTG 1380
 QY 1411 GCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTTCAGATAGAGAGGTTATCT 1470
 Db 1381 GCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTTCAGATAGAGAGGTTATCT 1440
 QY 1471 TGCTGATTTCAGGTGGGCCCAAAATATCACCACAAGGGTCTCTATTAAGAAAGGCGCAGAA 1530
 Db 1441 TGCTGATTTCAGGTGGGCCCAAAATATCACCACAAGGGTCTCTATTAAGAAAGGCGCAGAA 1500
 QY 1531 GGTCAAAGAGGTAGAGACAAAGTGTATGTAAGTGGAGCTGGTGGTGTGACGTGACGAGG 1590
 Db 1501 GGTCAAAGAGGTAGAGACAAAGTGTATGTAAGTGGAGCTGGTGGTGTGACGTGACGAGG 1560
 QY 1591 GCATGAAATGCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCCTGCTGG 1650
 Db 1561 GCATGAAATGCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCCTGCTGG 1620
 QY 1651 AGCTTCCAAAGAAACCCAGCCCTGCCAGCTTCACCTTGAGCCCATTTGAACTGATCTT 1710
 Db 1621 AGCTTCCAAAGAAACCCAGCCCTGCCAGCTTCACCTTGAGCCCATTTGAACTGATCTT 1680
 QY 1711 GAGTCTCTGGCTCCAGAAATTCAGAGAGAAATAAATTTGTTGTTTTTAAATGAAAAAAA 1770
 Db 1681 GAGTCTCTGGCTCCAGAAATTCAGAGAGAAATAAATTTGTTGTTTTTAAATGAAAAAAA 1740
 QY 1771 AAAAAAATAAAAAA 1786
 Db 1741 AAAAAAATAAAAAA 1756

RESULT 11

ADB80635
 ID ADB80635 standard; cDNA; 1837 BP.

XX ADB80635;

XX AC ADB80635;

XX DT 04-DEC-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO10111 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; gene; ss; cytosolic;
 XX KW vulvular; antiarthritic; pericyte cell proliferation;
 XX KW pericyte cell differentiation; chondrocyte cell proliferation;
 XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 XX KW gene therapy.

XX OS Homo sapiens.

XX PN US2003088068-A1.

XX PD 08-MAY-2003.

XX PF 13-AUG-2002; 2002US-00219481.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

QY 1411 GCAGAAAGGACAGTGCAGATGCTATGTAAGTTAAGGACTTTGAGATAGAGAGGTTATCT 1470
 Db 1381 GCAGAAAGGACAGTGCAGATGCTATGTAAGTTAAGGACTTTGAGATAGAGAGGTTATCT 1440
 QY 1471 TGTGATTCAGTGGGCCCCAAATATCACCAAGGGTCCCTATAGAAAGAGGCCAGAA 1530
 Db 1441 TGTGATTCAGTGGGCCCCAAATATCACCAAGGGTCCCTATAGAAAGAGGCCAGAA 1500
 QY 1531 GGTCAAGAGGTAGACACAAAGTATGATGGAAGTGGACGTGGGTGTCACGTGAGCAGGG 1590
 Db 1501 GGTCAAGAGGTAGACACAAAGTATGATGGAAGTGGACGTGGGTGTCACGTGAGCAGGG 1560
 QY 1591 GCCATGATGCCGACGCTTCAGATGCCAGAAAGGGAAGGATGATTCCTCCCTGCTGG 1650
 Db 1561 GCCATGATGCCGACGCTTCAGATGCCAGAAAGGGAAGGATGATTCCTCCCTGCTGG 1620
 QY 1651 AGCTCCCAAGAAACACGAGCCCTGCGCCAGCTTGACCTTGAGCCCATTTGAAACTGATCTT 1710
 Db 1621 AGCTCCCAAGAAACACGAGCCCTGCGCCAGCTTGACCTTGAGCCCATTTGAAACTGATCTT 1680
 QY 1711 GAGCTCCTGGCTCCAGATTCGAGGAGAAATATTTGTTGTTTAAATGAAAAAAA 1770
 Db 1681 GAGCTCCTGGCTCCAGATTCGAGGAGAAATATTTGTTGTTTAAATGAAAAAAA 1740
 QY 1771 AAAAAAAGAAAAA 1786
 Db 1741 AAAAAAAGAAAAA 1756

RESULT 12

ID ADB73176
 AC ADB73176;
 XX ADB73176;
 XX ADB73176;
 DT 04-DEC-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO101111 CDNA.

human; secreted and transmembrane protein; PRO; gene; ss; cytostatic;
 KW vulnary; antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.
 OS Homo sapiens.
 XX US2003096968-A1.
 XX 22-MAY-2003.
 XX 29-AUG-2002; 2002US-00232223.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski FJ;
 XX Gramaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-765525/72.
 XX P-PSDB; ADB73177.
 XX New isolated PRO polypeptides useful as molecular weight markers in
 XX protein electrophoresis, useful for tissue typing, and for treating
 XX arthritis and tumors.

XX PS Claim 2; Fig 39; 308pp; English.
 XX CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC priyete cells. PRO357, PRO229, PRO1272 or PRO405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1378, PRO1387, PRO1409, PRO1474, PRO1476, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptide
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This sequence encodes a human secreted and transmembrane
 CC PRO polypeptide.

SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 QY 32 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGTGCTCCAGGCTCCACTGAGGGGAAC 91
 Db 1 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGTGCTCCAGGCTCCACTGAGGGGAAC 60
 QY 92 GGGGACCTGTCTGAAGAGAGAGATGCCCTGTGACACTCTACCTGCTCTCTTCTGGCTC 151
 Db 61 GGGGACCTGTCTGAAGAGAGAGATGCCCTGTGACACTCTACCTGCTCTCTTCTGGCTC 120
 QY 152 TCAGGCTACTCCATTGCCACTCAATACCCGCTCCAAACAGTGAATGGTTGGAGCGG 211
 Db 121 TCAGGCTACTCCATTGCCACTCAATACCCGCTCCAAACAGTGAATGGTTGGAGCGG 180
 QY 212 GGCTCTTGAACCGTCAAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGGTG 271
 Db 181 GGCTCTTGAACCGTCAAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGGTG 240
 QY 272 TGTCGAGGAGCTATTGGCGTCAAGTGTGTTTAAACAGTGGGTTCAGAGCAG 331
 Db 241 TGTCGAGGAGCTATTGGCGTCAAGTGTGTTTAAACAGTGGGTTCAGAGCAG 300
 QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGCACGTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGCACGTTCACTGTG 360
 QY 392 ACCATGGAGGATCTCATGAAAACTGATCTGACACTTACTGTGGTGGTATGAAAACT 451
 Db 361 ACCATGGAGGATCTCATGAAAACTGATCTGACACTTACTGTGGTGGTATGAAAACT 420

alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1161, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1130, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO1934, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO329, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This sequence encodes a human secreted and transmembrane
CC PRO polypeptide.

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
XX
XX
SQ

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match	97.0%;	Score 1741.6;	DB 8;	Length 1837;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1749;	Conservative	6;	Mismatches 0;	Indels 1;
				Gaps 1;
QY	32	ACCAGCAGAAGGCTGGAGTCTGTAGTTTGTCTGCTGCAGGCTCCACTGAGGGGAAC	91	
DB	1	ACCAGCAGNAGGCTGGAGTCTGTAGTTTGTCTGCTGCCAGGCTTCACTGNGGGGAC	60	
QY	92	GGGGACCTGTCGTAAGAGAAAGATCCGCTGTGTGACATCTACTGCTCTCTTCTGGCTC	151	
DB	61	GGGGACCTGTCGTAAGAGAAAGATCCGCTGTGTGACATCTACTGCTCTCTTCTGGCTC	120	
QY	152	TCAGGCTACTCCATTGCCACTCAATCACCGTCCACACACAGTGAATGCGTTGGAGCGG	211	
DB	121	TCAGGCTACTCCATTGCCACTCAATCACCGTCCACACACAGTGAATGCGTTGGAGCGG	180	
QY	212	GGCTCCTTGAACGTCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	271	
DB	181	GGCTCCTTGAACGTCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	240	
QY	272	TGTCGAGAGACTATTGGCGTGACTGCAAGATCCTTGTTAAACACAGTGGGTGACAGAG	331	
DB	241	TGTCGAGAGACTATTGGCGTGACTGCAAGATCCTTGTTAAACACAGTGGGTGACAGAG	300	
QY	332	GAGGTGAAGAGGGAACCGGGTTCATCAAGACAATCAGAAAAACCGCACGTTCACTGTG	391	
DB	301	GAGGTGAAGAGGGAACCGGGTTCATCAAGACAATCAGAAAAACCGCACGTTCACTGTG	360	
QY	392	ACCATGGAGGATCTCATGAACACTGATCTGACACITACTGTGGTGTGGAAATCGGAAACT	451	
DB	361	ACCATGGAGGATCTCATGAACACTGATCTGACACITACTGTGGTGTGGAAATCGGAAACT	420	
QY	452	GGAAATGACCTTGGGGTCA CAGTTCAAGTGAACCATGACCCAGCACCTGACCCAGAA	511	
DB	421	GGAAATGACCTTGGGGTCA CAGTTCAAGTGAACCATGACCCAGCACCTGACCCAGAA	480	
QY	512	GAACTACAGCTCCCAACTCTGACCGGCCACCACTTGACACAGGACACAGCTCTG	571	
DB	481	GAACTACAGCTCCCAACTCTGACCGGCCACCACTTGACACAGGACACAGCTCTG	540	
QY	572	AAGCTCAGTGTCTCTGCCCTCATCTTCAACATATKTYGTGTGTTTTGTGTGCCGCC	631	

disorders (e.g. arthritis, sports injuries), involving inducing the re-
differentiation of chondrocytes. The PRO polypeptides are useful as
molecular markers for protein electrophoresis, and in tissue typing. This
sequence represents a human PRO polynucleotide of the invention.

XX
SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 9; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGAAAC 91
Db 1 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGAAAC 60

QY 92 GGGGACCTGTCTGAAGAGAAAGATGCTGTGACATCTACCTGCTCTCTTCTGGCTC 151
Db 61 GGGGACCTGTCTGAAGAGAAAGATGCTGTGACATCTACCTGCTCTCTTCTGGCTC 120

QY 152 TCAGGCTACTCCATTGCCACTCAATACCGGTCCACAAACAGTGAATGGCTTGAGCGG 211
Db 121 TCAGGCTACTCCATTGCCACTCAATACCGGTCCACAAACAGTGAATGGCTTGAGCGG 180

QY 212 GGCTCCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGG 271
Db 181 GGCTCCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGG 240

QY 272 TGTGAGAGGCTATTGCGGTGACTGCAAGATCTTGTATTAACAGTGGGTGAGAGG 331
Db 241 TGTGAGAGGCTATTGCGGTGACTGCAAGATCTTGTATTAACAGTGGGTGAGAGG 300

QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGGACGCTTCACTGTG 391
Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGGACGCTTCACTGTG 360

QY 392 ACCATGGAGATCTCATGAAACTGATGCTGACATTTACTGTGTGGAAATTGAGAAAACT 451
Db 361 ACCATGGAGATCTCATGAAACTGATGCTGACATTTACTGTGTGGAAATTGAGAAAACT 420

QY 452 CGAAATGACCTTGGGGTCAAGTTCAGTGCATTCAGCCAGCACCAAGTCCCAAGAA 511
Db 421 GGAATGACCTTGGGGTCAAGTTCAGTGCATTCAGCCAGCACCAAGTCCCAAGAA 480

QY 512 GAAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGACCAAGTCTCTG 571
Db 481 GAAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGACCAAGTCTCTG 540

QY 572 AAGCTCAGTGTCTCTGCGCTCATCTTCAACATATTTCTGCTGCTTTTGGTGGCGCC 631
Db 541 AAGCTCAGTGTCTCTGCGCTCATCTTCAACATATTTCTGCTGCTTTTGGTGGCGCC 600

QY 632 TCACCTCTTGGCTTGGAGATGATGAAGTACCAGCAGAAAGCAGCGCGGATGTCCCCAGAG 691
Db 601 TCACCTCTTGGCTTGGAGATGATGAAGTACCAGCAGAAAGCAGCGCGGATGTCCCCAGAG 660

QY 692 CAGGTACTGCAGCCCTTGAGGGCGGACCTCTGCTATGAGACCTGACCTGAGCTGGCC 751
Db 661 CAGGTACTGCAGCCCTTGAGGGCGGACCTCTGCTATGAGACCTGACCTGAGCTGGCC 720

QY 752 GGAACCTCCCGGAAAGGCTACCAAGAGCTTCTCTGCGCCAGGTTGACCAAGTGGAA 811
Db 721 GGAACCTCCCGGAAAGGCTACCAAGAGCTTCTCTGCGCCAGGTTGACCAAGTGGAA 780

QY 812 GTGGAATATGTCAACATGGCTTCTTGGCGAAGGAGACATTTCTATGCAATCTCTGACC 871
Db 781 GTGGAATATGTCAACATGGCTTCTTGGCGAAGGAGACATTTCTATGCAATCTCTGACC 840

QY 872 TTGGGTGCTGAGATCAGGAACCGGACCTACTGCAATGGGCGCACTCAGTAGCCAMCTY 931
Db 841 TTGGGTGCTGAGATCAGGAACCGGACCTACTGCAATGGGCGCACTCAGTAGCCAMCTY 900

QY 932 CCGGAGGCGGCGCTTGGAGGAGCCACCGAAATACAGCACCATCAGCAGGCTTAGCCTGCA 991

1711 GAGCTCTGCGCTCCAGATTGAGGAGATAAATTTGTTGTTTAAATGAAAAAAA 1770
1681 GAGCTCTGCGCTCCAGATTGAGGAGATAAATTTGTTGTTTAAATGAAAAAAA 1740

1771 AAAAAAAAAAAAAA 1786
1741 AAAAAAAAAAAAAA 1756

RESULT 14
ADB84906
ID ADB84906 standard; cDNA; 1837 BP.
XX AC ADB84906;
XX DT 04-DEC-2003 (first entry)
XX DE Human PRO polynucleotide #20.
XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
XX tumour; cancer; lung; colon; breast; prostate; rectum; liver;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
XX arthritis; sports injury; cytostatic; antiarthritic.
XX Homo sapiens.
OS
XX US2003073817-A1.
XX 17-APR-2003.
XX 26-AUG-2002; 2002US-00227883.
XX 01-AUG-2000; 2000US-0222425P.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaudi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-730024/69.
XX P-PSDB; ADB84907.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX e.g. in gene therapy, disease diagnosis, chromosome identification and
XX tissue typing.
XX Claim 2; Fig 39; 314pp; English.
XX The invention relates to human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the PRO polynucleotides encoding them.
XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. They are particularly useful for
XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
XX prostate tumour, rectal tumour or liver tumour) in a mammal, for
XX stimulating the release of tumour necrosis factor (TNF)-alpha from human
XX blood, for stimulating the proliferation or differentiation of
XX chondrocyte cells, for stimulating the proliferation of or gene
XX expression in pericyte cells or for stimulating the proliferation of
XX normal human dermal fibroblasts. The PRO nucleic acids are useful as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant
XX technology, in generating transgenic animals or knock-out animals which
XX may be used in the development and screening of therapeutically useful
XX reagents, in gene therapy, in chromosome identification, as chromosome
XX markers and in generating probes. The PRO polypeptides, or anti-PRO
XX antibodies, are useful for preparing a medicament for treating a
XX condition which is responsive to the PRO polypeptides or anti-PRO
XX antibodies, such as pericyte-associated tumours and bone and/or cartilage

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 16:38:22 ; Search time 139 Seconds

(without alignments)
7170.445 Million cell updates/sec

Title: US-09-997-131-19

Perfect score: 1796

Sequence: 1 ggaagaggaagtccaagg.....aaaaaaaaaagggcgccgc 1796

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	183.4	10.2	2345	3	US-08-955-937A-1
2	183.4	10.2	2345	3	US-09-300-985-1
3	176.2	9.8	708	3	US-08-955-937A-3
4	176.2	9.8	708	3	US-08-300-985-3
C 5	103	5.7	246240	2	US-08-724-394A-20
C 6	103	5.7	246240	2	US-08-724-394A-21
C 7	103	5.7	246240	2	US-08-724-394A-22
8	99.6	5.5	2103	2	US-08-897-340-2
9	99.6	5.5	2103	3	US-09-253-329-2
10	98.4	5.5	4079	4	US-09-016-434-1449
11	84.6	4.7	8758	4	US-09-793-345-3
12	84.6	4.7	8758	4	US-09-962-276-3
13	78.8	4.4	5445	4	US-09-578-458-15
C 14	75.8	4.2	128779	4	US-09-497-855A-38
15	75.6	4.2	998	4	US-09-316-081-1
16	75.6	4.2	998	4	US-09-316-081-3
17	75.6	4.2	998	4	US-09-578-458-1
18	75.6	4.2	998	4	US-09-578-458-3
19	75.6	4.2	998	4	US-09-522-964A-1
20	75.6	4.2	998	4	US-09-522-964A-3
C 21	75.4	4.2	432	4	US-09-621-976-9684
22	74	4.1	1366	4	US-09-578-458-12
23	74	4.1	1366	4	US-09-578-458-14
24	74	4.1	1366	4	US-09-522-964A-12
25	74	4.1	1366	4	US-09-522-964A-14
26	68.6	3.8	492	4	US-09-582-934-6
27	68.6	3.8	894	4	US-09-582-934-5

28	68.6	3.8	903	4	US-09-582-934-4	Sequence 4, Appli
C 29	66.6	3.7	148567	4	US-09-801-876B-3	Sequence 3, Appli
C 30	66.6	3.7	148567	4	US-10-254-869-3	Sequence 3, Appli
C 31	63.2	3.5	50000	4	US-09-146-053-4	Sequence 4, Appli
C 32	60.4	3.4	51719	4	US-09-918-686-2	Sequence 2, Appli
C 33	60.4	3.4	92139	4	US-09-918-686-1	Sequence 1, Appli
C 34	58.8	3.3	99500	4	US-09-738-096-10	Sequence 10, Appli
C 35	56.2	3.1	65042	4	US-09-784-316-3	Sequence 3, Appli
C 36	56.2	3.1	92139	4	US-09-918-886-1	Sequence 1, Appli
C 37	56	3.1	11703	3	US-09-101-886B-3	Sequence 3, Appli
C 38	55.6	3.1	460	1	US-08-474-542A-277	Sequence 277, App
C 39	55.6	3.1	460	1	US-08-232-463-14	Sequence 14, Appli
C 40	54	3.0	7218	1	US-08-457-648-277	Sequence 277, App
41	52	2.9	1200	1	US-08-592-126-125	Sequence 125, App
42	52	2.9	1200	4	US-09-158-595-125	Sequence 125, App
43	51.8	2.9	474	4	US-09-621-976-14736	Sequence 14736, A
C 44	51.4	2.9	176373	3	US-09-128-155-17	Sequence 17, Appli
45	51.2	2.9	261	4	US-09-621-976-18330	Sequence 18330, A

ALIGNMENTS

RESULT 1

US-08-955-937A-1
Sequence 1, Application US/08955937A
Patent No. 6020161
GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUNEH, ALEMGED
TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
TITLE OF INVENTION: GENE SUPERFAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,937A
FILING DATE: 17-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,152
FILING DATE: 19-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846189
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-955-937A-1

Query Match 10.2%; Score 183.4; DB 3; Length 2345;
Best Local Similarity 70.7%; Pred. No. 5.1e-41;
Matches 258; Conservative 0; Mismatches 106; Indels 1;
Gaps 1;

Db 236 GGAGACCTACATTAAAGTGGTGGTCCCGAGGGGTGGCTGGGATACATGCAAGATCCCTCAT 295
Qy 310 TAAACACAGTGGGTACAGAGGAGGTGAAGAGGACCGGTGTCCATCAAGGACAATCA 369
Db 296 TGAACACAGAGGTGGAGGACAGAGAGAGAGTGAACCGTGTCCATCAAGGACAATCA 355
Qy 370 GAAAAACCGCACGTTTCACTGTGACCATGGAGGATCTCATGAAAACTGATGTCGACATTA 429
Db 356 GAAAGACCGCACGTTTCACTGTGACCATGGAGGATCTCATGAAAACTGATGTCGACATTA 415
Qy 430 CTGGTGTGGAATTGAGAAAACTGAAATGACCTTTGGGTGACAGTTCAGGTGACCATTTGA 489
Db 416 CTGGTGTGGAATTGAGAAAACTGAAATGACCTTTGGGTGACAGTTCAGGTGACCATTTGA 475
Qy 490 CCCAGACCACTGACCCCAAGAGAACTAGCAGCTCCCACTCTGACCGGCCCACTT 549
Db 476 ACCAGAGGAGCGGCTTTCCACACAGCAAGCTCACTACCAACAGCAATATGGCAGT 535
Qy 550 GGACAAACAGGACAAAGCTCTTGAAGCTCAGTGTCTCTCTGCTCCCTCATCTTACCATATT 609
Db 536 GTTCATCGGCTCCCAAGAGAACTACATGCTCTCTGATTTGTGAAGGTGCCCAT 595
Qy 610 KYTGTGCTTTTGGTGGCGCTCACTCTTG 640
Db 596 CTTCATCTTTGGTCAATGCAATCTCTGG 626

RESULT 5
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA

Db 176 GTCTGTGAGAGCCCAAGAGAGGGTCCCTGAGGTTCAATGCCACTATAACCAAGGATG 235
Qy 250 GGAGACCTACTTTAAAGTGTGTGTCGAGGAGCTATTTGGCGTGTGACTGCAAGATCCCTGT 309
Db 236 GGAGACCTACTTTAAAGTGTGTGTCGAGGAGTTCGCTGGGATACATGCAAGATCCCTCAT 295
Qy 310 TAAACACAGTGGGTACAGAGGAGGTGAAGAGGACCGGTGTCCATCAAGGACAATCA 369
Db 296 TGAACACAGAGGTGGAGGACAGAGAGAGAGTGAACCGTGTCTCATCAAGGACAATCA 355
Qy 370 GAAAAACCGCACGTTTCACTGTGACCATGGAGGATCTCATGAAAACTGATGTCGACATTA 429
Db 356 GAAAGACCGCACGTTTCACTGTGACCATGGAGGATCTCATGAAAACTGATGTCGACATTA 415
Qy 430 CTGGTGTGGAATTGAGAAAACTGAAATGACCTTTGGGTGACAGTTCAGGTGACCATTTGA 489
Db 416 CTGGTGTGGAATTGAGAAAACTGAAATGACCTTTGGGTGACAGTTCAGGTGACCATTTGA 475
Qy 490 CCCAGACCACTGACCCCAAGAGAACTAGCAGCTCCCACTCTGACCGGCCCACTT 549
Db 476 ACCAGAGGAGCGGCTTTCCACACAGCAAGCTCACTACCAACAGCAATATGGCAGT 535
Qy 550 GGACAAACAGGACAAAGCTCTTGAAGCTCAGTGTCTCTCTGCTCCCTCATCTTACCATATT 609
Db 536 GTTCATCGGCTCCCAAGAGAACTACATGCTCTCTGATTTGTGAAGGTGCCCAT 595
Qy 610 KYTGTGCTTTTGGTGGCGCTCACTCTTG 640
Db 596 CTTCATCTTTGGTCAATGCAATCTCTGG 626

RESULT 4
US-09-300-985-3
; Sequence 3, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALIEMSEED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: FIGR-1 A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 708
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (475) (620) (660)
US-09-300-985-3

Query Match 9.8%; Score 176.2; DB 3; Length 708;
Best Local Similarity 59.9%; Pred. No. 2.6e-39;
Matches 306; Conservative 2; Mismatches 202; Indels 1; Gaps 1;
Qy 130 CTACCTGTCTCTTCTGCTCTCAGGCTACTCCATTCGCACTCAAAATCACCGGTCCAAAC 189
Db 117 CTGCCCCCTGCTCTGCTCTCTCAGCTCTCAGGCTGTCTC-CATCCAGGCGCCAGA 175
Qy 190 AACAGTGAATGGTTGGAGCGGGCTCTTGACCGGTGAGTGTGTTACAGATCAGGCTG 249
Db 176 GTCTGTGAGAGCCCCAGAGAGGGGTCCCTGACCGTTCAATGCCACTATAGCAAGGATG 235
Qy 250 GGAGACCTACTTTGAAAGTGGTGTGTCGAGGAGCTATTTGGCGTGTGCTGCAAGATCCTTGT 309

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; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
; US-08-724-394A-20

Query Match      5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;

QY 1341 TGGGCTGAATAATGGCCCCCAAGGATATCTGTGCTCTAATCTCAGAACTTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127
QY 1401 ACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAG 1460
Db 37126 TTACCTTATATGACAAAGGAGACTTTACATGTTTAAATAGTTAAGATTTTGAGATGGC 37067
QY 1461 AGGTTATCTTCTGATTCAGTGGCCCCCAAAATATCACCACAGGGTCTCATAAGAA 1520
Db 37066 AGATTTTCTGAAATTTTGAGATGGCCCC-TAGTGTAAATCAAGGGTCTCTTAAGAGA 37008
QY 1521 GAGGCCAGAGTCAAGAGGTAGAGACA-----AAGTGATGATGGAAGTGGACGT 1571
Db 37007 CAGGCAGAGAGTCAAGATAAGAGAAAAATACTTCAAGATGTTACACTGTGGCTTTAAG 36948
QY 1572 GGGTGTGACGTGAGCAGGGCCATGATGCCAGGAAACCAAGCCCTGCCACGCCCTTGACTTGA 1631
Db 36947 GTGGAGGAAAGGCCAAGAGCCAAAAAATGTCAGTGGTCACTACAAGCTGAAAGAAAGA 36888
QY 1632 AATGATTTCCCTGCTGAGTCCCAAGAAACCAAGCCCTGCCACGCCCTTGACTTGA 1691
Db 36828 GCTCAGTGAACCCATTTTGACCTTCTGACCTTTAGAAATTTGTAATAATAATAATTTT 36769
QY 1752 TGTGTTTT 1758
Db 36768 GTGTTGT 36762

RESULT 6
US-08-724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
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```
;
;
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
; US-08-724-394A-21

Query Match      5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;

QY 1341 TGGGCTGAATAATGGCCCCCAAGGATATCTGTGCTCTAATCTCAGAACTTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127
QY 1401 ACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAG 1460
Db 37126 TTACCTTATATGACAAAGGAGACTTTACATGTTTAAATAGTTAAGATTTTGAGATGGC 37067
QY 1461 AGGTTATCTTCTGATTCAGTGGCCCCCAAAATATCACCACAGGGTCTCATAAGAA 1520
Db 37066 AGATTTTCTGAAATTTTGAGATGGCCCC-TAGTGTAAATCAAGGGTCTCTTAAGAGA 37008
QY 1521 GAGGCCAGAGTCAAGAGGTAGAGACA-----AAGTGATGATGGAAGTGGACGT 1571
Db 37007 CAGGCAGAGAGTCAAGATAAGAGAAAAATACTTCAAGATGTTACACTGTGGCTTTAAG 36948
QY 1572 GGGTGTGACGTGAGCAGGGCCATGATGCCAGGAAACCAAGCCCTGCCACGCCCTTGACTTGA 1631
Db 36947 GTGGAGGAAAGGCCAAGAGCCAAAAAATGTCAGTGGTCACTACAAGCTGAAAGAAAGA 36888
QY 1632 AATGATTTCCCTGCTGAGTCCCAAGAAACCAAGCCCTGCCACGCCCTTGACTTGA 1691
Db 36887 AATGGATTTTCCCTTAAAGCCCTCTGGAGGGGCA-CAACCTTGCCAAATACCTTGATTTG 36829
QY 1692 GCCATTGAAACTGATCTTGAGCTCCCTGGCCCTCAGAAATTCAGGAGAAATAAATTTTGT 1751
Db 36828 GCTCAGTGAACCCATTTTGACCTTCTGACCTTTAGAAATTTGTAATAATAATAATTTT 36769
QY 1752 TGTGTTTT 1758
Db 36768 GTGTTGT 36762

RESULT 7
US-08-724-394A-22/c
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
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RESULT 8
US-08-897-340-2
; Sequence 2, Application US/08897340
; Patent No. 5955306
; GENERAL INFORMATION:
; APPLICANT: Gimero, Carlos J. and Errada, Patrick. R.
; TITLE OF INVENTION: Weight Control Pathway Genes and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,340
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/715,032
; FILING DATE: 17-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-005CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2103 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-897-340-2

Query Match 5.5%; Score 99.6; DB 2; Length 2103;
Best Local Similarity 57.0%; Pred. No. 1.3e-17;
Matches 285; Conservative 0; Mismatches 199; Indels 16; Gaps 5;
QY 1286 TGAAGTACCATTATCATATAACAA TGAACCTTTATTTATGCTTACCACATGTTATGGGC 1345
Db 1611 TGAACACCAAACTATTATACGGAGGGTGAATAGTTTTCGTCCTCCAGTTGTGGTAGG 1670
QY 1346 TGAATATGCCCCCAAGATATCTGTGTCCTAAATCCTCAGAACTTGTCACCTTTACCTT 1405
Db 1671 CCAGTAGTGGCTCCCAAGATGCCCATGTCCTTAATCCAGGAACTGTCAAATTTACCTT 1730
QY 1406 CTCTGCAGAAAAGGACAGTGCAGATGTATGTAAGTTAAAGACTTTTGATAGATGAGAGGT 1465
Db 1731 GTATGCCC-AAAGGGCTTTGCAGATGTAAATGAAGTTAAGGATCTTTCGCCAGGAAGAT 1789
QY 1466 ATTCTTTGATTCAGTGGGCCCAAAATATACACAAGGGTCTCTCATAGAAGAGGC 1525
Db 1790 ATCCAGCTTTTCAGAGGGCTTTGATGTCCTCACCGGGTCTGTATATACAGAGAGCAG 1849
QY 1526 CAGAAGTCAAAGAGGTAGAGACAAAGTGTATGTAAGTGAAGTGAAGTGGGTGTGACGTGAG 1585
Db 1950 GTACGGGAGAGAGGTG-----GAGGTGTAGCGATGGACAGAGAACTGGAGTTGA 1902
QY 1586 CAGGGCCATGAATGCGCGAGCCTTCAGATGCCAGAAAGGAAAGGATGGATTCCTCCCTG 1645
Db 1903 GGAGGGCAGCTCAAGCCACAGAGTCCAGGCGACCTCAGAGCCAGGAAATGCAAT---CCCTC 1959
QY 1646 CCTGGAGCTCCAAAGAAACCAGCCCTGCCCCGCTTGACITTAGCCCCCAATGAAACTG 1705

US-08-724-394A-22
Query Match 5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;
QY 1341 TGGGCTGAATAATGCCCCCAAGATATCTGTGCTCTAACTCCTCAGAACTTTGACATGTT 1400
Db 37186 TAGGCTGAATGTTGCTCTCCAAAGATATCCATGCTCTAAATCCCAAGACCTGTAAATATA 37127
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QY 1461 AGGTATTTCTTCTGATTTCAGTGGGCCCAAAATATCACCAAGGGTCTCTCAAGAAA 1520
Db 37066 AGATTTTCTGAAATTTTCAGATGGGCC--TAGTGTATATCAAGGGTCTCTATAGAGA 37008
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Db 36947 GTGAGGAAAGGCCAAGAGCCAAAATAATGCAAGTGTGCTCACTCAAGCTGAAAGAAAGAA 36888
QY 1632 AATGATTTCCCTGCTGAGGCTCCAAAAGAAAACAGCCCTGCCCAGCCCTTGACATTGA 1691
Db 36887 AATGATTTTCCCTTAAGCCTCTGGAGGGGCA--CAACCTTGCAATACCTTTGATTTG 36829
QY 1692 GCCCATTAAGATGATCTGAGCTCTGCGCTCCAGAAATTCAGAGAGATTAATTTGTGT 1751
Db 36828 GCTCAGTGAAGCCCATTTTGACCTTTGACCTTTAGAAATTTGAAATAAATAAATAATTTT 36769
QY 1752 TGTTTT 1758
Db 36768 GTGTGT 36762

Db 1960 CCACAGAGCCCTGGAGGCCCGCCCTGCTCCACCTGGACT--GGCTCAGTAGGCTA 2017
QY 1706 ATCTTGAGCTCCTGGC---CTCCAGAAATTCAGGAGGATAAATTTGCTGTTTAAATG 1762
Db 2018 ATTTTATAATTCGCTGATTTTAAACTCTAAGGAAATTAATTTGTGTGTTTAAATC 2077
QY 1763 AAAAAAAAAAAAAAAAAAAAAA 1782
Db 2078 AAAAAAAAAAAAAAAAAAAAAA 2097

RESULT 9

US-09-252-329-2
; Sequence 2, Application US/09252329
; Patent No. 6147192
; GENERAL INFORMATION:
; APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
; TITLE OF INVENTION: Weight Control Pathway Genes and Uses
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/252,329
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,340
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-005CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2103 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-09-252-329-2

Query Match 5.5%; Score 99.6; DB 3; Length 2103;
Best Local Similarity 57.0%; Pred. No. 1.3e-17;
Matches 285; Conservative 0; Mismatches 199; Indels 16; Gaps 5;
QY 1286 TGAAGTACCATATCATATACATGACCTTTATTTATGCTTACCATCATGTTATGGC 1345
Db 1611 TGAACACCAAACTATATACCGAGGGGTGAATAGTTTGTGCGCCAGTTGTGTAG 1670
QY 1346 TGAATAATGGCCCCCAAGATATCTGTCTCTATCTCAGAACTGTGACTTTACCTT 1405
Db 1671 CCAGTAGTGGCTCCCAAGATGCCATGTCCTATCCAGCACTGTCAAAATTTACCTT 1730
QY 1406 CTGTGGCAGAGGAGGACGATGATGTAAGTTAAGGACTTTGAGATAGAGGTT 1465
Db 1731 GTATGGCC-AAAGGGGCTTTTGCAGATGTAATGAAGTTAAGGATCTTTCGCCAGAGATT 1789
QY 1466 ATTCTTCTGATTCAGTGGGCCCAAAATATCACCACAGGGTCTCTCATAGAAAGAGGC 1525

Db 1790 ATCCAGCTGTTTCAGGAGGGCTTGATGCTCTCACCCGGTCTGTATAACAGAGAGCAG 1849
QY 1526 CAGAGGTCAAGAGAGTAGACAAAGTATGATGGAAGTGACGCTGGGTGACGTGAG 1585
Db 1850 GTACGGGAGAGAGAGTTG-----GAGGTGTAGCATGAGGAGCAAGAACTGGAGTTGA 1902
QY 1586 CAGGGCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAATGGATTCCTCCCTG 1645
Db 1903 GGAGGGCAGCTCAAGCCACAGAGTCCAGGCCACCTCAGAGCCAGGAATGCAAT--CCTC 1959
QY 1646 CTTGGAGCCTCCAAAGAAACAGCCCTGCCACGCTTGACTTGAGCCCATGAAATG 1705
Db 1960 CCACAGAGCCTGGAAAGGCCCCAGCCCTGCTCCACCTGGACT--GGCTCAGTAGGCTA 2017
QY 1706 ATCTTGAGCTCCTGGC---CTCCAGAAATTCAGGAGGATAAATTTGCTGTTTAAATG 1762
Db 2018 ATTTTATAATTCGCTGATTTTAAACTCTAAGGAAATTAATTTGTGTGTTTAAATC 2077
QY 1763 AAAAAAAAAAAAAAAAAAAAAA 1782
Db 2078 AAAAAAAAAAAAAAAAAAAAAA 2097

RESULT 10

US-09-016-434-1449
; Sequence 1449, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1449:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G727358
; US-09-016-434-1449

Query Match

5.5%; Score 98.4; DB 4; Length 4079;

Best Local Similarity 60.2%; Pred. No. 4.2e-17;
Matches 201; Conservative 0; Mismatches 126; Indels 7; Gaps 2;

Qy 1430 ATGTATGTAAGTAAAGACCTTTGAGATAGACAGATTATCTTCTGATTCAGGTGGGCC 1489
Db 3712 ATGTTACCAATTAAGGCTCTTGGATGGGAGATGATCTGATATCAAGTGGGCC 3771
Qy 1490 AATAATACACAAAGGCTCTTATAGAAAGAGGCCAGAGTCAAGAGGTAGAGACA 1549
Db 3772 -TATATAATCACAAAGGCTCTTATAGAGAGAGGCCAGGAGGCTCAGAGTATGT 3829
Qy 1550 AAGTGATGATGGAAGTGAAGTGGTGTGAGCTGAGCA-----GGGSCCATGAATGCCG 1604
Db 3830 GACTATGAGACAGAGCCAGAGAAATCAGGACGGCCACTAGAGCCAGGATTCGAGG 3889
Qy 1605 AGCCTTCAGATGCCAGAAAGGGAAGGAATGGATTCCTCCCTGCTGAGCCCTCAAAAGAA 1664
Db 3890 CACCCTCTAGAGGCTGTAAAGGCAAGAAATGGCTTCTCCCTGAGGCTCCAGAAGGA 3949
Qy 1665 ACAGCCCTGCCACGCTTGAATGAGCCCATTTGAATGAACTGATCTTGAAGTCTGCGCTC 1724
Db 3950 ATGGGTCTGCTGCAACTCCCTGTCTTCAGCCAGGAAACAGATTTAGGATTTCTGGCCTC 4009
Qy 1725 CAGAAATGCAGGAGATAAATTTGTGTGTTTTT 1758
Db 4010 CAGAACTGTAGAGATACATTTGTGTGTTTT 4043

RESULT 11
US-09-799-345-3
; Sequence 3, Application US/09799345
; Patent No. 6323016
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001156
; CURRENT APPLICATION NUMBER: US/09/799,345
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8758
; TYPE: DNA
; ORGANISM: Human
US-09-799-345-3

Query Match 4.7%; Score 84.6; DB 4; Length 8758;
Best Local Similarity 69.3%; Pred. No. 4.8e-13;
Matches 115; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1603 GCAGCCTTCAGATGCCAGAAAGGGAAGGAATGGATTCCTCCCTGCTGAGCCCTCAAAAG 1662
Db 3859 GCGGCCACAGACCTGAAATGTTAGGACATGATGTTCTCCCTCAGAGCTCCAAAG 3918
Qy 1663 AAACAGCCCTGCCACGCTTGAATGAGCCCATTTGAAATGATCTTGAAGTCTGCGCC 1722
Db 3919 AAAACAGTCTCTGACACCTTGAATGAGCCAGTGAAGTGGCTTTGGGCTTCTGACC 3978
Qy 1723 TCCAGAAATGCAGGAGATAAATTTGTGTGTTTTTAAATGAAAAA 1768
Db 3979 TCCAGAACTGTAAACAGAAAAATAATGTGTGTTTTTAAAGCCACTAAA 4024

TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001156DIV
CURRENT APPLICATION NUMBER: US/09/962,276
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/210,458
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/799,345
PRIOR FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8758
TYPE: DNA
ORGANISM: Human
US-09-962-276-3

Query Match 4.7%; Score 84.6; DB 4; Length 8758;
Best Local Similarity 69.3%; Pred. No. 4.8e-13;
Matches 115; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1603 GCAGCCTTCAGATGCCAGAAAGGGAAGGAATGGATTCCTCCCTGCTGAGCCCTCAAAAG 1662
Db 3859 GCGGCCACAGACCTGAAATGTTAGGACATGATGTTCTCCCTCAGAGCTCCAAAG 3918
Qy 1663 AAACAGCCCTGCCACGCTTGAATGAGCCCATTTGAAATGATCTTGAAGTCTGCGCC 1722
Db 3919 AAAACAGTCTCTGACACCTTGAATGAGCCAGTGAAGTGGCTTTGGGCTTCTGACC 3978
Qy 1723 TCCAGAAATGCAGGAGATAAATTTGTGTGTTTTTAAATGAAAAA 1768
Db 3979 TCCAGAACTGTAAACAGAAAAATAATGTGTGTTTTTAAAGCCACTAAA 4024

TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001156DIV
CURRENT APPLICATION NUMBER: US/09/962,276
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/210,458
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/799,345
PRIOR FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8758
TYPE: DNA
ORGANISM: Human
US-09-962-276-3

Query Match 4.4%; Score 78.8; DB 4; Length 5445;
Best Local Similarity 54.0%; Pred. No. 1.5e-11;
Matches 230; Conservative 0; Mismatches 187; Indels 9; Gaps 3;

Qy 1336 TGTATGGCTGAATTAATGCCCCC-AAAGATATCTGTCTCTTAATCTCAGACTTGTG 1394
Db 5023 TATGGTAGGAGAAATAATGCCCCGAAATATGTCCACATCTTAATCCCAAGATCTGTC 5082
Qy 1395 ACTGTTACCTTCTGTGCGAGAAAGGACAGATGATGTAGTTAAGGACTTTGAG 1454
Db 5083 ATATGTTACATACATGTCCTCAAGAGGTTTTCGAATGTGATTATGTTAAGGATCTTGA 5142
Qy 1455 ATAGAGAGTTATCTTGTGATGAGTGGGCCCCAAAATATCACCAAGGGTCTCAT 1514

Db 5143 ATGAGGAGCAATCTCTGGGTTATCTCTTGGGCTCAGTTTAAATCACAAGAGGAGGAGG 5202
QY 1515 AAGAAAGAGGCGAGAGGTCAGAGAGGTCAGACAAAGTGTATGATGGAAGTCGACGTGGG 1574
Db 5203 AAGGGAGAGTCAGAGAGAGATGGAAGATACCATGCTTCTAATTTTGAAGAT-----GG 5256
QY 1575 TGTGACGTGAGCAGGGGCGATGAATGCCGCGACCTTCAGATGCCAGAAAGGGAAGGAAT 1634
Db 5257 AGTGAGGGGCGCTTGAGCCAAACAAATGCAGGTGTTTTAGAGGTGGGAAAGCCAGGGAA 5316
QY 1635 CGATTCCCTGCTGGAGCCTCCAAAGAAACAGCCCTGCCAGCCCTTGACCTTGAGCC 1694
Db 5317 CGGATTCTCTCTAGAGTCTCCGGAAGGAACACAGCTCT--TGACACATGATTTGAGCT 5374
QY 1695 CATGGAAGTCTTGAGCTCTGCTGCTCCAGATTCAGAGAGATGAGAGATGATTTGTTGT 1754
Db 5375 CAGTGACACCCATTTGAGCTCTGACCTCCACAACTATAAAATAAATGTTGTTAT 5434
QY 1755 TTTTAA 1760
Db 5435 TGTAAA 5440

RESULT 14
US-09-497-855A-38/c
; Sequence 38, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-38

Query Match 4.2%; Score 75.8; DB 4; Length 128779;
Best Local Similarity 57.2%; Pred. No. 7e-10;
Matches 242; Conservative 0; Mismatches 162; Indels 19; Gaps 5;
QY 1349 ATAATGGCCCCCAAGATATCTGTGCTCTAATCTCTCAGAACTTGACTGTACTTCTG 1408
Db 9626 AAAATGCCCCCAAGATATCCATGCTCTAATCTTGGAACTCTCTGAATATTACCTTACT 96207
QY 1409 TGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGACCTTCAGATAGAGGTTATT 1468
Db 96206 TTGCACAGACCCCAAGGGGGTCT--TCGGAAGAAAGTTAAGATGAGAAATTATC 96148
QY 1469 CTGCTGATTCAGGTGGGCCCAAAATATACCAACAAGGTCCTCATGAAGAAAGGCCAG 1528
Db 96147 CTGGATTATCCAAAGTGGAGCTCAAAATACCATCAAGTGCCCTTTAAATAGGAGAGGCACA 96088
QY 1529 AAGGTCA-----AAGAGGTAGACAAAGTGTATGATGGAAGTGGCGTGGGT 1575
Db 96087 GGGAGATTATACAGTTACAGAAAGAGAAAGACAAATGTGACCAACCGGACACAGATGAA 96028
QY 1576 GTGACGTGAGAGGGGCCATGAATGCC--GCAGCTTTCAGATGCCAGAAAGGGAAGGAA 1633
Db 96027 GCAATGCCACCAACAGCCAGGAATCGAGCAGCCACAGAGGCTGGGAAAAGTGAAGGA 95968
QY 1634 TGGATTCCTCTGCTGGAGCTCCAAAGAAACC--AGCCCTGCCAGCCCTGACTTGAG 1692
Db 95967 CATATTTCTC--CTTAGAGCTCCGGAGGGAGCATAGCCCTGCCCAACACCTTGATTCAA 95910

QY 1693 CCATTGAAACTGATCTTGAGCTCCTGGCTCCAGAAATTCAGAGGAGATAAATTTGTGT 1752
Db 95909 ACCAGTGATACTGAGTTTGGACTTTTGGCTCCAGAACTGTGAGAAAGAGGTCACCTAT 95850
QY 1753 GTT 1755
Db 95849 TTT 95847

RESULT 15
US-09-316-081-1
; Sequence 1, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(512)
US-09-316-081-1

Query Match 4.2%; Score 75.6; DB 4; Length 998;
Best Local Similarity 53.5%; Pred. No. 4.3e-11;
Matches 228; Conservative 0; Mismatches 189; Indels 9; Gaps 3;
QY 1336 TGTATGGGCTGAATAATGGCCCCC-AAAGATATCTGTGCTCTAATCTCTCAGAACTTGTG 1394
Db 574 TATGTTAGGCAGATAAATGTCCTCCGAAATATGTCCACATCCTAATCCCAAGATCTGTGC 633
QY 1395 ACTGTTACCTTCTGTGGCAGAAAGGACAGTCAGATGTATGTAAGTTAAGGACTTTGAG 1454
Db 634 ATATGTTACCATACATGTCCAAAGAGTTTGCAAATGTGATTATGTTAAGATCTTGA 693
QY 1455 ATAGAGAGTTATTTCTGCTGATTGAGTGGGCCCAAAATATCACCAGGGTCTCAT 1514
Db 694 ATGAGGAGACAATCTCTGGGTTATCTCTTGGGCTCAGTTTAAATCACAAGAGGAGGAGG 753
QY 1515 AAGAAAGAGGCCAGAGGTCAAAGAGGTAGAGACAAAGTGTATGTAAGTGGAGCTGGG 1574
Db 754 AAGGAGAGTTCAGAGAGAGATGGAAGATACCATGCTTCTTAATTTGAAGAT-----GG 807
QY 1575 TGTGACGTGAGCAGGGGCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAAT 1634
Db 808 AGTGAGGGGCTTGAGCCAAACATATGTCAGGTGTTTTTAGAAGAGGAGGAGGAGGAA 867
QY 1635 GGAATCCCTGCTGAGGCTCCAAAGAAACCAGCCCTGCCAGCCCTGACTTTGAGCC 1694
Db 868 CGGATTCCTCTATAGTCTCCGGAAGGAACACAGCTCT--TGACATGATGATTTGAGCT 925
QY 1695 CATTGAAACTGATCTTTGAGCTCCTGCCCTCCAGAAATTCAGAGAGATAAATTTGTGTGT 1754
Db 926 CAGTGACACCCATTTGAGCTTCTGACCTCCACACTATAAAATAATAAATTTGTGTAT 985
QY 1755 TTTTAA 1760
Db 986 TGTAAA 991

Search completed: September 21, 2004, 20:41:10
Job time : 142 secs


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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-535-39

Query Match          97.0%; Score 1741.6; DB 13; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGAGTCTGTAGTTTCTGCTGCCAGGCTCCACTGAGGGGAAC 91
DB 1 ACCAGCAGAGGCTGGAGTCTGTAGTTTCTGCTGCCAGGCTCCACTGAGGGGAAC 60

QY 92 GGGGACCTGTCTGAGAGAGAGTGCCTCTGCTGACACTCTACCTGCTCTCTCTGCTC 151
DB 61 GGGGACCTGTCTGAGAGAGAGTGCCTCTGCTGACACTCTACCTGCTCTCTCTGCTC 120

QY 152 TCAGGCTACTCTCATTCGCCACTCAATACACCGGTCCAAACAGAGTAATGGCTTGGAGCGG 211
DB 121 TCAGGCTACTCTCATTCGCCACTCAATACACCGGTCCAAACAGAGTAATGGCTTGGAGCGG 180

QY 212 GGCTCCTTGACCGTGCAGTGTGTTTACAGATAGGCTGGGAGACCTACTTGAATGTGTG 271
DB 181 GGCTCCTTGACCGTGCAGTGTGTTTACAGATAGGCTGGGAGACCTACTTGAATGTGTG 240

QY 272 TGTCCAGGAGCTATTGTGCTGACTGCAAGATCCTTGTATTAACAGTGGTTCAGAGCAG 331
DB 241 TGTCCAGGAGCTATTGTGCTGACTGCAAGATCCTTGTATTAACAGTGGTTCAGAGCAG 300

QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCCGACGTTCACTGTG 391
DB 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCCGACGTTCACTGTG 360

QY 392 ACCATGGAGATCTCATGAAACTGATGCTGACACTTACTGTTGTAATGAGAAACT 451
DB 361 ACCATGGAGATCTCATGAAACTGATGCTGACACTTACTGTTGTAATGAGAAACT 420

QY 452 GGAATGCACTTTGGGTCACAGTTCAGTACCATTGACCCAGCACCAAGTCAACCAAGAA 511
DB 421 GGAATGCACTTTGGGTCACAGTTCAGTACCATTGACCCAGCACCAAGTCAACCAAGAA 480

QY 512 GAACTAGCAGTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGCAAGCTCTTG 571
DB 481 GAACTAGCAGTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGCAAGCTCTTG 540

QY 572 AAGCTCACTGTCTCTGCCCTCATCTTACCATAATTKYTGTCCTTTTGGTGGCCGCC 631
DB 541 AAGCTCACTGTCTCTGCCCTCATCTTACCATAATTKYTGTCCTTTTGGTGGCCGCC 600

QY 632 TCACCTTTGGCTTGGAGATGATGAAGTACAGAGAAAGCAGCGCGGATGTCCCAAGAG 691
DB 601 TCACCTTTGGCTTGGAGATGATGAAGTACAGAGAAAGCAGCGCGGATGTCCCAAGAG 660

QY 692 CAGGTACTGACGCCCTCGAGGGCGACTCTGCTATGACACCTGACCCCTGACGCTGGCC 751
DB 661 CAGGTACTGACGCCCTCGAGGGCGACTCTGCTATGACACCTGACCCCTGACGCTGGCC 720

QY 752 GGAACCTCCCGGAAAGGCTTACCAGAAAGCTTCTCTGCCAGGTTGACCAAGTGGAA 811
DB 721 GGAACCTCCCGGAAAGGCTTACCAGAAAGCTTCTCTGCCAGGTTGACCAAGTGGAA 780

QY 812 GTGGATATGTGACATGGCTCTCTTCCCGAGGAGGACATTTCTTATGATCTTGACC 871
DB 781 GTGGATATGTGACATGGCTCTCTTCCCGAGGAGGACATTTCTTATGATCTTGACC 840

QY 872 TTGGTGTCTGAGGATCAGGAACCGACCTACTGCAACATGGGCCCACTCAGTAGCCAMCTY 931
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DB 841 TTGGGTGCTGAGGATCAGGAACCGAAGCTACTGCAACATGGGCCACCTCAGTAGCCACCTC 900
QY 932 CCGGAGAGGGGCTCAGGAGCCCGGGAATACAGCAACATCAGCAGGCTTAGCCTGCA 991
DB 901 CCGGAGAGGGGCTCAGGAGCCCGGGAATACAGCAACATCAGCAGGCTTAGCCTGCA 960
QY 992 CTCAGGCTCCTTTCTTGGACCCCGAGGCTGTGACACACTCTGCTCCTCATCGACCGCTCTGC 1051
DB 961 CTCAGGCTCCTTTCTTGGACCCCGAGGCTGTGACACACTCTGCTCCTCATCGACCGCTCTGC 1020
QY 1052 CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGGTCTGCTGCTCATCAGCAGCA 1111
DB 1021 CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGGTCTGCTGCTCATCAGCAGCA 1080
QY 1112 TTGCCCCTAGCTGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1171
DB 1081 TTGCCCCTAGCTGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1140
QY 1172 TTTTCTAAAGCTCCCTCTCTCT-CTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG 1230
DB 1141 TTTTCTAAAGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1231 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTATTCATGAAG 1290
DB 1201 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTATTCATGAAG 1260
QY 1291 TACCATATCAATAACAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1350
DB 1261 TACCATATCAATAACAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1320
QY 1351 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1410
DB 1321 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
QY 1411 GCAGAAAGGACAGTCAGATGTATGTAAGTTAAGGACTTTTGAGATAGAGAGGTTATTTCT 1470
DB 1381 GCAGAAAGGACAGTCAGATGTATGTAAGTTAAGGACTTTTGAGATAGAGAGGTTATTTCT 1440
QY 1471 TGCTGATTCAGTGGGCCCAAAATATACCAACAGGGTCTCTATGAAGAGGCCAGAA 1530
DB 1441 TGCTGATTCAGTGGGCCCAAAATATACCAACAGGGTCTCTATGAAGAGGCCAGAA 1500
QY 1531 GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1590
DB 1501 GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1560
QY 1591 GGCATGATTCGCGACCTTTCAGATGCGAGAAAGGAAAGGAAATGGATTCCTGCTCTGG 1650
DB 1561 GGCATGATTCGCGACCTTTCAGATGCGAGAAAGGAAAGGAAATGGATTCCTGCTCTGG 1620
QY 1651 AGCTCTCCAAAAGAAACCCAGCCCTGCCCGCTTCACTTGAGCCCATTTGAAACTGATCTT 1710
DB 1621 AGCTCTCCAAAAGAAACCCAGCCCTGCCCGCTTCACTTGAGCCCATTTGAAACTGATCTT 1680
QY 1711 GAGCTCTGCTGCTCAGAAATTCAGAGGAATAAATTTCTGTGTTTTTAAATGAAAAAAA 1770
DB 1681 GAGCTCTGCTGCTCAGAAATTCAGAGGAATAAATTTCTGTGTTTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAGAAAAA 1786
DB 1741 AAAAAAAGAAAAA 1756
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RESULT 2

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US-10-232-230-39
; Sequence 39, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
```

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C103
CURRENT APPLICATION NUMBER: US/10/232,230
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 39
LENGTH: 1837
TYPE: DNA
ORGANISM: Homo Sapien
us-10-232-230-39

Query Match 97.0%; Score 1741.6; DB 13; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

Qy	32	ACGAGAGAGGCTGGAGCTGTAGTTTCTCTGCTGCCAGGCTCCACTGAGGGGAC	91
Db	1	ACCGAGAGAGGCTGGAGCTGTAGTTTCTCTGCTGCCAGGCTCCACTGAGGGGAC	60
Qy	92	GGGACCTGTCTGAAGAGAGATGCCCTCTGTGACACTCTACCTGTCTCTCTCTGCTC	151
Db	61	GGGACCTGTCTGAAGAGAGATGCCCTCTGTGACACTCTACCTGTCTCTCTCTGCTC	120
Qy	152	TCAGGCTACTCCATGTCACCTAAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCG	211
Db	121	TCAGGCTACTCCATGTCACCTAAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCG	180
Qy	212	GGCTCCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTACTTGAAGTGTGG	271
Db	181	GGCTCCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTACTTGAAGTGTGG	240
Qy	272	TGTCAGGAGCTATTTGGCGTCACTGCAAGATCCTTTAAACCACTGGGTGAGCAG	331
Db	241	TGTCAGGAGCTATTTGGCGTCACTGCAAGATCCTTTAAACCACTGGGTGAGCAG	300
Qy	332	GAGGTGAAGAGGACCGGTCTCCATCAAGACAAATCAGAAACCCGACCTTCACTGTG	391
Db	301	GAGGTGAAGAGGACCGGTCTCCATCAAGACAAATCAGAAACCCGACCTTCACTGTG	360
Qy	392	ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGGAATTGAAAACT	451
Db	361	ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGGAATTGAAAACT	420
Qy	452	GAAATGACCTTGGGGTCAAGTTCAGTACCATTGACCCAGCACCAGTCCACCAAGAA	511

Db	421	GGAAATGACCTTGGGGTCAAGTTCAGTTCACCAATGACCAAGACCAAGTCCACCAAGAA	480
Qy	512	GAAATGACCTTGGGGTCAAGTTCAGTTCACCAATGACCAAGACCAAGTCCACCAAGT	571
Db	481	GAAATGACCTTGGGGTCAAGTTCAGTTCACCAATGACCAAGACCAAGTCCACCAAGT	540
Qy	572	AAGCTAGTGTCTCTGCGCCCTCATCTTACCAATATKTYTGTCTTTTGGTGGCGCC	631
Db	541	AAGCTAGTGTCTCTGCGCCCTCATCTTACCAATATKTYTGTCTTTTGGTGGCGCC	600
Qy	632	TCACCTTGGCTTGGAGATGATGAAGTACAGCAGAAAGACAGCCGGATGTCCCCAGAG	691
Db	601	TCACCTTGGCTTGGAGATGATGAAGTACAGCAGAAAGACAGCCGGATGTCCCCAGAG	660
Qy	692	CAGTACTGACGCCCTTGGAGGCGACTCTGTATGACACCTGACCCCTGACGTGGCC	751
Db	661	CAGTACTGACGCCCTTGGAGGCGACTCTGTATGACACCTGACCCCTGACGTGGCC	720
Qy	752	GGAACCTCCCGGAAAGGCTACCAAGAGCTTCTCTGCCAGAGTGGACCAAGTGGAA	811
Db	721	GGAACCTCCCGGAAAGGCTACCAAGAGCTTCTCTGCCAGAGTGGACCAAGTGGAA	780
Qy	812	GTGGAATATGTCAACATGGCTTCTCTGCCAGAGGAGACATTTCTATGCAATCTGACC	871
Db	781	GTGGAATATGTCAACATGGCTTCTCTGCCAGAGGAGACATTTCTATGCAATCTGACC	840
Qy	872	TTGGTGTGAGGATCAGGAAACCGACCTACTGCAACATGGGCCCAACCTCAGTAGCCACTY	931
Db	841	TTGGTGTGAGGATCAGGAAACCGACCTACTGCAACATGGGCCCAACCTCAGTAGCCACTY	900
Qy	932	CCCGCAGGGGCGCTGAGGAGCCACCGAATACAGCACCATCAGCAGCCCTTAGCCTGCA	991
Db	901	CCCGCAGGGGCGCTGAGGAGCCACCGAATACAGCACCATCAGCAGCCCTTAGCCTGCA	960
Qy	992	CTCCAGGCTCTCTTGGAAACCCAGGCTGTGAGCACACTCTCTGCTCATGACACCTCTGC	1051
Db	961	CTCCAGGCTCTCTTGGAAACCCAGGCTGTGAGCACACTCTCTGCTCATGACACCTCTGC	1020
Qy	1052	CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTCTGCTGATCAGCAGCA	1111
Db	1021	CCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTCTGCTGATCAGCAGCA	1080
Qy	1112	TTGCCCTAGCTCTGGTGGGCTTTGGGCGCAAGTCTCAGGGGGCTTTAGAGTTGGG	1171
Db	1081	TTGCCCTAGCTCTGGTGGGCTTTGGGCGCAAGTCTCAGGGGGCTTTAGAGTTGGG	1140
Qy	1172	TTTTCTAAAGCTCCCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG	1230
Db	1141	TTTTCTAAAGCTCCCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG	1200
Qy	1231	GGCTTTTCATGGGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATG	1290
Db	1201	GGCTTTTCATGGGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATG	1260
Qy	1291	TACCATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	1350
Db	1261	TACCATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	1320
Qy	1351	AATGGCCCCCAAGATATCTGTCTAATCTCTCAGAACTTGTGACTGTGACTGTGACTGTG	1410
Db	1321	AATGGCCCCCAAGATATCTGTCTAATCTCTCAGAACTTGTGACTGTGACTGTGACTGTG	1380
Qy	1411	GCAGAAAGGAGACATGACATCTATGTAAGTTAAAGACTTTGAGATAGAGGTTATTCT	1470
Db	1381	GCAGAAAGGAGACATGACATCTATGTAAGTTAAAGACTTTGAGATAGAGGTTATTCT	1440
Qy	1471	TGCTGATTGAGTGGGCCCAAAATATCAACAGGCTCTCATAGAAAGAGGCGCAGAA	1530
Db	1441	TGCTGATTGAGTGGGCCCAAAATATCAACAGGCTCTCATAGAAAGAGGCGCAGAA	1500
Qy	1531	GGTCAAGAGGTAGAGCAAAAGTGTGATGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG	1590

Db 1081 TTGCCCTAGCTCTGGGTTGGGCTTGGGCCAAGTCTCAGGGGGCTTCTAGAGTTGGG 1140
Qy 1172 TTTTCTAAAGCTCCCTCTCT-CTACATAGTTAGGGGGGCTAGGATATGCTCTGG 1230
Db 1141 TTTTCTAAAGCTCCCTCTCTCTCTACATAGTTAGGGGGGCTAGGATATGCTCTGG 1200
Qy 1231 GGCTTTTATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTTATCATGAAG 1290
Db 1201 GGCTTTTATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTTATCATGAAG 1260
Qy 1291 TACATATCATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1350
Db 1261 TACATATCATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1320
Qy 1351 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1410
Db 1321 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Qy 1411 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
Db 1381 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1471 TGCTGATTCAGGTGGGCCCCCAATATCACCACAGGCTCCTCATAAGAGAGGCCAGAA 1530
Db 1441 TGCTGATTCAGGTGGGCCCCCAATATCACCACAGGCTCCTCATAAGAGAGGCCAGAA 1500
Qy 1531 GGTCAAGAGGTAGACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
Db 1501 GGTCAAGAGGTAGACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 1591 GCATGATTCAGGCGGCTTCAGATGCCAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1650
Db 1561 GCATGATTCAGGCGGCTTCAGATGCCAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1620
Qy 1651 AGCTTCCAAAGAAACAGCGCTGCCACGCTTGAATTCAGGCGGCTTGAATTCAGGCGGCTT 1710
Db 1621 AGCTTCCAAAGAAACAGCGCTGCCACGCTTGAATTCAGGCGGCTTGAATTCAGGCGGCTT 1680
Qy 1711 GAGCTCTGGCTCCAGAAATGAGAGGAAATGATGATGATGATGATGATGATGATGATGAT 1770
Db 1681 GAGCTCTGGCTCCAGAAATGAGAGGAAATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1771 AAAAAAAAAAAAAA 1786
Db 1741 AAAAAAAAAAAAAA 1756

RESULT 4
US-10-227-884-39
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; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ACIDS AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287

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Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY	32	ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGTGCTCCAGGCTCCACTGAGGGGAAC	91
DB	1	ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGTGCTCCAGGCTCCACTGAGGGGAAC	60
QY	92	GGGACCTGTCTGAAGAGAAGATGCCCTGTGTGACACTTCTACCTGCTCTCTTTCTGGCTC	151
DB	61	GGGACCTGTCTGAAGAGAAGATGCCCTGTGTGACACTTCTACCTGCTCTCTTTCTGGCTC	120
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QY	272	TGTCAGAGAGTATTGGCGTGACTGCAAGATCCTTGTAAACCAAGTGGTTCAGAGCAG	331
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QY	452	GGAAATGACCTTGGGGTCACAGTTCAAGTGACCATTCAGCCAGACCCAGTCCACCAAGAA	511
DB	421	GGAAATGACCTTGGGGTCACAGTTCAAGTGACCATTCAGCCAGACCCAGTCCACCAAGAA	480
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DB	481	GAAGTACAGCTCCCAACTTCTGACCGGCAACACTTGGACAACAGGCAAGCTCCTG	540
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 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

32 ACCAGCAGAGGCTGGAGTCTGTAGTTTCTGTCAGGCTCCACTGAGGGAAC 91

QY

|||||

1 ACCAGCAGAAAGGCTGGAGACTCTGTAGTTTGTTCCTGCTGCCAGGCTCCACTGAGGGGAC 60
92 GGAGACCTGTCTGAAGAGAGAGAGTGGCCCTGCTGACACCTCTACCTGCTCTCTCTTCTGGGTC 151
61 GGAGACCTGTCTGAAGAGAGAGTGGCCCTGCTGACACCTCTACCTGCTCTCTCTTCTGGGTC 120
152 TCAGGCTACTCCATTCGCACTCAATACAGGCTCCAGCAACAGTGAATGGCTTGGAGGG 211
121 TCAGGCTACTCCATTCGCACTCAATACAGGCTCCAGCAACAGTGAATGGCTTGGAGGG 180
212 GGCTCCTTGACCGCTGAGTGTGTTTACAGATCAGGCTGGAGACCTTACCTTGAAGTGGTGG 271
181 GGCTCCTTGACCGCTGAGTGTGTTTACAGATCAGGCTGGAGACCTTACCTTGAAGTGGTGG 240
272 TGTGAGGAGCTATTTGGCGTACTGCAAGTCTTGTGTTAAACACAGTGGGTGAGAGAG 331
241 TGTGAGGAGCTATTTGGCGTACTGCAAGTCTTGTGTTAAACACAGTGGGTGAGAGAG 300
332 GAGGTGAAGGAGCAGGCTGCTCAATCAGGCAATCAGAAACAGCAGCTTCACTGTG 391
301 GAGGTGAAGGAGCAGGCTGCTCAATCAGGCAATCAGAAACAGCAGCTTCACTGTG 360
392 ACCATGAGGATCTCATGAAAACTGATGTGACACTTACTGTGTGGAATTGAAAACT 451
361 ACCATGAGGATCTCATGAAAACTGATGTGACACTTACTGTGTGGAATTGAAAACT 420
452 GGAATGACCTTGGGTGACAGTTCAGTACCATTTGACCCAGCAGCTCAGCCAGAA 511
421 GGAATGACCTTGGGTGACAGTTCAGTACCATTTGACCCAGCAGCTCAGCCAGAA 480
512 GAAACTAGCAGCTCCCCAACTCTGACCGGCGACACTTTGACACACAGGCAACAGCTCCTG 571
481 GAACTAGCAGCTCCCCAACTCTGACCGGCGACACTTTGACACACAGGCAACAGCTCCTG 540
572 AAGCTAGTGTCTCTGCGCCCTCATCTTCAACATATKTYGTGCTTTTGTGGCGGC 631
541 AAGCTAGTGTCTCTGCGCCCTCATCTTCAACATATKTYGTGCTTTTGTGGCGGC 600
632 TCACCTTGTGGCTTGAGAGATGATGAGTACAGCAGAAACAGCAGGAGTGTCCACAG 691
601 TCACCTTGTGGCTTGAGAGATGATGAGTACAGCAGAAACAGCAGGAGTGTCCACAG 660
692 CAGTACTGACGCGCTGGAGGCGACCTCTGTATGACACCTGACCCCTGAGCTGGCC 751
661 CAGTACTGACGCGCTGGAGGCGACCTCTGTATGACACCTGACCCCTGAGCTGGCC 720
752 GGAACTCCCGCGAAAGGCTTACCAGAACTTCTCTGCGCAGGTTGACAGGTGGAA 811
721 GGAACTCCCGCGAAAGGCTTACCAGAACTTCTCTGCGCAGGTTGACAGGTGGAA 780
812 GTGGAATATGTACACATGGCTTCTTCCGGAAGGAGGACATTTCTATGATCTCTGACC 871
781 GTGGAATATGTACACATGGCTTCTTCCGGAAGGAGGACATTTCTATGATCTCTGACC 840
872 TTGGGTGCTGAGGATCAGGAAACCGACCTTACTGCAACATGCGGCACTCAGTAGCCACTY 931
841 TTGGGTGCTGAGGATCAGGAAACCGACCTTACTGCAACATGCGGCACTCAGTAGCCACTY 900
932 CCGGCGAGGCGCTGAGGAGCCACAGGATACAGCAGCCTTACAGGCGCTTACCTGCA 991
901 CCGGCGAGGCGCTGAGGAGCCACAGGATACAGCAGCCTTACAGGCGCTTACCTGCA 960
992 CTCACAGGCTCTCTTGGACCCCGAGGCTGTGAGCAGACTCTGTGCTCATGACCGCTGTC 1051
961 CTCACAGGCTCTCTTGGACCCCGAGGCTGTGAGCAGACTCTGTGCTCATGACCGCTGTC 1020
1052 CCCCTGCTCCCTCATCAGGACCCACCGGCGACTGTGCTCTCTGCTGATCAGCCAGCA 1111
1021 CCCCTGCTCCCTCATCAGGACCCACCGGCGACTGTGCTCTCTGCTGATCAGCCAGCA 1080
1112 TTGCCCCCTAGCTCTGGGTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGAGTTGGG 1171
1081 TTGCCCCCTAGCTCTGGGTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGAGTTGGG 1140

1172 TTTTCTAAACGTCCCTCTCTCTCTCATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230
1141 TTTTCTAAACGTCCCTCTCTCTCTCATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1200
1231 GGCCTTTCATGGAATGATGAAGATGATTAATGAGAAAAATGTTATCATATTATCATGAAG 1290
1201 GGCCTTTCATGGAATGATGAAGATGATTAATGAGAAAAATGTTATCATATTATCATGAAG 1260
1291 TACCATTTATCATATACAAATGAACTTTTATTTGCTTACCTACCATCTTATGGGCTGAAT 1350
1261 TACCATTTATCATATACAAATGAACTTTTATTTATTTGCTTACCTACCATCTTATGGGCTGAAT 1320
1351 AATGGCCCCCAAGATATCTGTGCTCTTAATCCTCAGAACTTTGACTGTTACCTTCTGTG 1410
1321 AATGGCCCCCAAGATATCTGTGCTCTTAATCCTCAGAACTTTGACTGTTACCTTCTGTG 1380
1411 GCAGAAAGGACAGTGCAGATGATGATTAAGTAAAGGACTTTGAGATAGAGAGTATTTCT 1470
1381 GCAGAAAGGACAGTGCAGATGATGATTAAGTAAAGGACTTTGAGATAGAGAGTATTTCT 1440
1471 TGCTGATTCAGTGGGGCCCCAAATATCACCAGAGGCTCTCTAAGAAAGAGGCCAGAA 1530
1441 TGCTGATTCAGTGGGGCCCCAAATATCACCAGAGGCTCTCTAAGAAAGAGGCCAGAA 1500
1531 GGTCAAAGAGGTAGAGACAAAGTATGATGAAAGTGAAGTGGGTGTCACCTGAGCAGGG 1590
1501 GGTCAAAGAGGTAGAGACAAAGTATGATGAAAGTGAAGTGGGTGTCACCTGAGCAGGG 1560
1591 GCCATGATTCGGCAGCCTTCAGATGCCAGAAAGGAAAGGATGGATTCCCTGCGCTGG 1650
1561 GCCATGATTCGGCAGCCTTCAGATGCCAGAAAGGAAAGGATGGATTCCCTGCGCTGG 1620
1651 AGCCTCCAAAAGAAACACAGCCTTCCCAAGCCTTGTGAGCCCATTTGAAACCTGATCTT 1710
1621 AGCCTCCAAAAGAAACACAGCCTTCCCAAGCCTTGTGAGCCCATTTGAAACCTGATCTT 1680
1711 GAGCTCCTGGCTCCAGAAATTCAGAGAGAAATAATTTGCTGTTTAAATGAAAAAAA 1770
1681 GAGCTCCTGGCTCCAGAAATTCAGAGAGAAATAATTTGCTGTTTAAATGAAAAAAA 1740
1771 AAAAAAAGAAAAA 1786
1741 AAAAAAAGAAAAA 1756

RESULT 6

US-10-230-338-39
; Sequence 39, Application US/10230338
; Publication No. US2003004934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILLING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILLING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILLING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILLING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILLING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILLING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILLING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-230-338-39

Query Match          97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTCTGCTGCAGGCTCCACTGAGGGGAAC 91
Db 1 ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTCTGCTGCAGGCTCCACTGAGGGGAAC 60

QY 92 GGGGACCTGTCTGAAGAAAGATGCCCTGTGTGACACTCTACCTGCTCTCTTCTGCTC 151
Db 61 GGGGACCTGTCTGAAGAAAGATGCCCTGTGTGACACTCTACCTGCTCTCTTCTGCTC 120

QY 152 TCAGCTACTCCATGCCACTCRAATCACCGGTCCACACAGTGAATGCTTGGAGCGG 211
Db 121 TCAGCTACTCCATGCCACTCRAATCACCGGTCCACACAGTGAATGCTTGGAGCGG 180

QY 212 GGCTCTTTGACCGTGCAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 271
Db 181 GGCTCTTTGACCGTGCAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 240

QY 272 TGTGAGGAGTATTTGGCTGACTGCAAGATCCTTGTAAACACAGTGGGTGAGAGCAG 331
Db 241 TGTGAGGAGTATTTGGCTGACTGCAAGATCCTTGTAAACACAGTGGGTGAGAGCAG 300

QY 332 CAGGTGAAGAGGGACCGGGTGTCCATCAAGGACAATCAGAAACACCGAGTTTCACTGTG 391
Db 301 CAGGTGAAGAGGGACCGGGTGTCCATCAAGGACAATCAGAAACACCGAGTTTCACTGTG 360

QY 392 ACCATGAGAGTATCATGAAACCTGATGCTGACACTTACTGGTGTGAATGAGAAACT 451
Db 361 ACCATGAGAGTATCATGAAACCTGATGCTGACACTTACTGGTGTGAATGAGAAACT 420

QY 452 GGAATGACCTTTGGGGTCACAGTTCAAGTGAACCAATTGACCCAGCACAGTCCACCAAGAA 511
Db 421 GGAATGACCTTTGGGGTCACAGTTCAAGTGAACCAATTGACCCAGCACAGTCCACCAAGAA 480

QY 512 GAAACTAGAGCTCCCAACTCTGACCGGCCACCACTTGGACACAGGCAACAAGCTCCTG 571
Db 481 GAAACTAGAGCTCCCAACTCTGACCGGCCACCACTTGGACACAGGCAACAAGCTCCTG 540

QY 572 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKVTGTGCTTTTGTGGCGGCC 631
Db 541 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKVTGTGCTTTTGTGGCGGCC 600

QY 632 TCACTCTTGGCTTGGAGGATGATGAAGTACCAGAGAAAGACCGCGGATGTCCCCAGAG 691
Db 601 TCACTCTTGGCTTGGAGGATGATGAAGTACCAGAGAAAGACCGCGGATGTCCCCAGAG 660

QY 692 CAGGTACTGACCCCTGGAGGGGACCTCTGTATGACAGACTGACCTGAGCTGGCC 751
Db 661 CAGGTACTGACCCCTGGAGGGGACCTCTGTATGACAGACTGACCTGAGCTGGCC 720

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QY 752 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTTCTCTGCCAGGTTGACCAAGTGGAA 811
Db 721 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTTCTCTGCCAGGTTGACCAAGTGGAA 780

QY 812 GTGGAATATGTCAACATGCTTCTTCCGAGAGGAGCAATTTCTATGCATCTCTGACC 871
Db 781 GTGGAATATGTCAACATGCTTCTTCCGAGAGGAGCAATTTCTATGCATCTCTGACC 840

QY 872 TTGGGTGCTGAGGATCAGGAACCGACTACTCTGCAACATGGGCACTCAGTAGCCAMCTY 931
Db 841 TTGGGTGCTGAGGATCAGGAACCGACTACTCTGCAACATGGGCACTCAGTAGCCAMCTY 900

QY 932 CCGCGAGGGGCTCTGAGAGGCCACGGAATACAGCAACATCAGCAGGCTTGTAGCTGCA 991
Db 901 CCGCGAGGGGCTCTGAGAGGCCACGGAATACAGCAACATCAGCAGGCTTGTAGCTGCA 960

QY 992 CTCAGGCTCCTTCTTGGAGCCAGGCTGTGAGCACACTCTGCTCATGAGCCGCTCTGC 1051
Db 961 CTCAGGCTCCTTCTTGGAGCCAGGCTGTGAGCACACTCTGCTCATGAGCCGCTCTGC 1020

QY 1052 CCCCTGCTCCCTCATCAGGACCAACCCGGGACTGGTGCCTCTCTGATCAGCAGCA 1111
Db 1021 CCCCTGCTCCCTCATCAGGACCAACCCGGGACTGGTGCCTCTCTGATCAGCAGCA 1080

QY 1112 TTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTGGG 1171
Db 1081 TTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTGGG 1140

QY 1172 TTTTCTAAACGTCCTCTCTCT - CTACATAGTTGAGAGGGGGCTTAGGGATATGCTCTGG 1230
Db 1141 TTTTCTAAACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

QY 1231 GGCTTTCATGGAATGATGAAGATGATTAAGAAAAATGTTATCATTTATCATGAAG 1290
Db 1201 GGCTTTCATGGAATGATGAAGATGATTAAGAAAAATGTTATCATTTATCATGAAG 1260

QY 1291 TACCATTTATATAACAAATGAACTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1350
Db 1261 TACCATTTATATAACAAATGAACTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1320

QY 1351 AATGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
Db 1321 AATGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGTGACTGTTACCTTCTGTG 1380

QY 1411 GCAGAAAGGACAGTGACAGATGATTAAGTAAAGTAAAGGACTTTGAGATAGAGGTTATCT 1470
Db 1381 GCAGAAAGGACAGTGACAGATGATTAAGTAAAGTAAAGGACTTTGAGATAGAGGTTATCT 1440

QY 1471 TGCTCATTTGAGTGGGCCCCAAAATATACCAAGGGTCTCTATAAGAAAGAGCCAGAA 1530
Db 1441 TGCTCATTTGAGTGGGCCCCAAAATATACCAAGGGTCTCTATAAGAAAGAGCCAGAA 1500

QY 1531 GGTCAAGAGGTAGAGACAAAGTGAATGAACTGGAAGTGAAGTGGTGTGACCTGAGCAGGG 1590
Db 1501 GGTCAAGAGGTAGAGACAAAGTGAATGAACTGGAAGTGAAGTGGTGTGACCTGAGCAGGG 1560

QY 1591 GCCATGAATGCCGAGCCTTCCAGATGCCAGAAAGGAAAGAAATGGATTCCTCTGCTCTGG 1650
Db 1561 GCCATGAATGCCGAGCCTTCCAGATGCCAGAAAGGAAAGAAATGGATTCCTCTGCTCTGG 1620

QY 1651 AGCTTCCAAAAGAAACAGCCCTGCCACGCTTGAAGTCTTGAAGCCCATGAACTGATCTT 1710
Db 1621 AGCTTCCAAAAGAAACAGCCCTGCCACGCTTGAAGTCTTGAAGCCCATGAACTGATCTT 1680

QY 1711 GAGCTCTCTGGCTCCAGAAATGAGAGGAAATTAATTTGTGTTTGTATGAAAAAAA 1770
Db 1681 GAGCTCTCTGGCTCCAGAAATGAGAGGAAATTAATTTGTGTTTGTATGAAAAAAA 1740

QY 1771 AAAAAAAGAAAAA 1786
Db 1741 AAAAAAAGAAAAA 1756

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RESULT_7

US-10-218-631-39
; Sequence 39, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auetin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: F530PIC14

CURRENT APPLICATION NUMBER: US/10/218,631

CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 39

; LENGTH: 1837

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-218-631-39

QY 992 CTCAGGCTCTTCTGGACCCAGGCTGTGAGCACATCTCTGCTCATGACCGTCTGC 1051
Db 961 CTCAGGCTCTTCTGGACCCAGGCTGTGAGCACATCTCTGCTCATGACCGTCTGC 1020
QY 1052 CCCTCTCTCCCTCATCAGGACCAACCCGGGACCTGGTCTCTGCTCTGATCAGCCAGCA 1111
Db 1021 CCCTCTCTCCCTCATCAGGACCAACCCGGGACCTGGTCTCTGCTCTGATCAGCCAGCA 1080
QY 1112 TTGCCCCAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGAGTTGGG 1171
Db 1081 TTGCCCCAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGAGTTGGG 1140
QY 1172 TTTTCTAAACGCTCCCTG 1230
Db 1141 TTTTCTAAACGCTCCCTG 1200
QY 1231 GGGTTTCATGGGAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1290
Db 1201 GGGTTTCATGGGAATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1291 TACCATTATCATAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1350
Db 1261 TACCATTATCATAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1351 AATGGCCCCAAAGATATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1410
Db 1321 AATGGCCCCAAAGATATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1380
QY 1411 GCAGAAAGGAGCAGTGCAGATCTATGTAAGTTAAGGACTTTGAGATGAGAGGTTATCT 1470
Db 1381 GCAGAAAGGAGCAGTGCAGATCTATGTAAGTTAAGGACTTTGAGATGAGAGGTTATCT 1440
QY 1471 TGGTGTATTCAGTGGGCCCCAAATATCACCAGGCTCTCATGAGAGGCCCCAGAA 1530
Db 1441 TGGTGTATTCAGTGGGCCCCAAATATCACCAGGCTCTCATGAGAGGCCCCAGAA 1500
QY 1531 GGTCAAGAGGTAGAGACAAAGTATGATGAGAGTGGAGCTGGTGTGACGTGAGCAGGG 1590
Db 1501 GGTCAAGAGGTAGAGACAAAGTATGATGAGAGTGGAGCTGGTGTGACGTGAGCAGGG 1560
QY 1591 GGCATGATGCGCGAGCCTTCAGATGCGAGAAAGGAAAGTATGATGATGATGATGATGATG 1650
Db 1561 GGCATGATGCGCGAGCCTTCAGATGCGAGAAAGGAAAGTATGATGATGATGATGATGATG 1620
QY 1651 AGCTCTCAAAAGAAACCGCCCTGCCACGCTTGACTTGAGCCCATTTGAACCTGATCTT 1710
Db 1621 AGCTCTCAAAAGAAACCGCCCTGCCACGCTTGACTTGAGCCCATTTGAACCTGATCTT 1680
QY 1711 GAGCTCTGGCTCCAGAAATTCAGAGAAATTAATTTGTTGTTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCTGGCTCCAGAAATTCAGAGAAATTAATTTGTTGTTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAAAAAAAAAAAA 1786
Db 1741 AAAAAAAAAAAAAAAAAA 1756

RESULT 9

US-10-216-159A-39
; Sequence 39, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-159A-39

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCACGACGAGCGTGGAGTCTGTAGTTGTTCTGCTGCGAGCTCCATGAGGGGAAAC 91
Db 1 ACCACGACGAGCGTGGAGTCTGTAGTTGTTCTGCTGCGAGCTCCATGAGGGGAAAC 60
QY 92 GGGGACCTGTCTGAAGAGAGAGTCCCTCTGTGACACTCTACCTGCTCTCTCTCTGCTC 151
Db 61 GGGGACCTGTCTGAAGAGAGAGTCCCTCTGTGACACTCTACCTGCTCTCTCTCTGCTC 120
QY 152 TCAGGCTACTCCATGCGCTCAATCAGCGTCCACACACAGTGAATGCTGGAGCGG 211
Db 121 TCAGGCTACTCCATGCGCTCAATCAGCGTCCACACACAGTGAATGCTGGAGCGG 180
QY 212 GCGTCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 271
Db 181 GCGTCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 240
QY 272 TGTGAGGAGTATTGGCGTGACTGCAAGATCTTGTAAACACAGTGGTCAAGCAG 331
Db 241 TGTGAGGAGTATTGGCGTGACTGCAAGATCTTGTAAACACAGTGGTCAAGCAG 300
QY 332 GAGGTGAAGAGGAGCGCGGTGTCCATCAAGCAATCAGAAACACCGACGTTCACTGTG 391
Db 301 GAGGTGAAGAGGAGCGCGGTGTCCATCAAGCAATCAGAAACACCGACGTTCACTGTG 360
QY 392 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTGCTGGAATGAGAAACT 451
Db 361 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTGCTGGAATGAGAAACT 420
QY 452 GGAATGACCTTTGGGGTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 511
Db 421 GGAATGACCTTTGGGGTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 480
QY 512 GAACTAGCAGTCCCCACTCTGACCGGCCACCGCTTGGACACAGGCAAGCTCTCTG 571
Db 481 GAACTAGCAGTCCCCACTCTGACCGGCCACCGCTTGGACACAGGCAAGCTCTCTG 540

QY 572 AAGCTCAGTGTCTCTGTCGCCCTCACTCTCAACATATTKYGTGCTTTTGTGTCGCCGCC 631
DB 541 AAGCTCAGTGTCTCTGTCGCCCTCACTCTCAACATATTKYGTGCTTTTGTGTCGCCGCC 600
QY 632 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
DB 601 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 692 CAGGTAAGTACAGCCCTGAGAGGCGACCTCTGCTATGAGAGACCTGACCTGTCAGCTGGCC 751
DB 661 CAGGTAAGTACAGCCCTGAGAGGCGACCTCTGCTATGAGAGACCTGACCTGTCAGCTGGCC 720
QY 752 GGAACCTCCCGGAGAGAGTACAGAGAGCTTCTCTGCCAGGTTGACAGAGTGAA 811
DB 721 GGAACCTCCCGGAGAGAGTACAGAGAGCTTCTCTGCCAGGTTGACAGAGTGAA 780
QY 812 GTGGAATATGTCAACATGCTTCTTGGCGAGAGAGACATTTCTATGCACTCTGACC 871
DB 781 GTGGAATATGTCAACATGCTTCTTGGCGAGAGAGACATTTCTATGCACTCTGACC 840
QY 872 TTGGGTGCTGAGGATCAGAAACCGACCTACTGCAACATGGGCCCACTCAGTAGCAGCTY 931
DB 841 TTGGGTGCTGAGGATCAGAAACCGACCTACTGCAACATGGGCCCACTCAGTAGCAGCTY 900
QY 932 CCGGCGAGGGGCGCTGAGAGGCGGACCGAATACAGCACCACAGAGGCTTTAGCCTGCA 991
DB 901 CCGGCGAGGGGCGCTGAGAGGCGGACCGAATACAGCACCACAGAGGCTTTAGCCTGCA 960
QY 992 CTCAGGCTCTCTTTGAGACCCAGGCTGTGAGCACACTCTGCTCATGACAGCTGTC 1051
DB 961 CTCAGGCTCTCTTTGAGACCCAGGCTGTGAGCACACTCTGCTCATGACAGCTGTC 1020
QY 1052 CCCCTGCTCCCTCATCAGGACCCAGGCGGAGCTGTGCTCTCTGCTGATCAGCAGCA 1111
DB 1021 CCCCTGCTCCCTCATCAGGACCCAGGCGGAGCTGTGCTCTCTGCTGATCAGCAGCA 1080
QY 1112 TTGCCCTAGCTCTGGTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1171
DB 1081 TTGCCCTAGCTCTGGTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1140
QY 1172 TTTTCTAAAGTCCCTCTCT-CTACATGTTGAGAGGGGGCTAGGATATGCTCTGG 1230
DB 1141 TTTTCTAAAGTCCCTCTCTCTACATGTTGAGAGGGGGCTAGGATATGCTCTGG 1200
QY 1231 GCGTTTTCATGGGAATGATGAAGATGAATAGAGAAAATGTTATCATTAATCATGAAG 1290
DB 1201 GCGTTTTCATGGGAATGATGAAGATGAATAGAGAAAATGTTATCATTAATCATGAAG 1260
QY 1291 TACCATTAATCATGAAGACCTTTATTTATGCTTACCAATGTTATGGGCTGAAT 1350
DB 1261 TACCATTAATCATGAAGACCTTTATTTATGCTTACCAATGTTATGGGCTGAAT 1320
QY 1351 AATGGCCCCAAGATATCTGTCTTAATCCCTCAGAACTTGTGCTTACCTCTGTCG 1410
DB 1321 AATGGCCCCAAGATATCTGTCTTAATCCCTCAGAACTTGTGCTTACCTCTGTCG 1380
QY 1411 GCAGAAAGGGACAGTGCAGATGATGAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1470
DB 1381 GCAGAAAGGGACAGTGCAGATGATGAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1440
QY 1471 TGCTGATTCAGGTGGGCGGCAATATACCAAGGCTCTCATAGAAAGAGGCGCAGAA 1530
DB 1441 TGCTGATTCAGGTGGGCGGCAATATACCAAGGCTCTCATAGAAAGAGGCGCAGAA 1500
QY 1531 GGTCAAAAGAGTGAAGAAAGTGAATGAGAAAGTGAAGTGGGTGACGTGAGCAGGG 1590
DB 1501 GGTCAAAAGAGTGAAGAAAGTGAATGAGAAAGTGAAGTGGGTGACGTGAGCAGGG 1560
QY 1591 GCCATGAATGCCGAGCCTTCAGATGCCAAGAGGAAAGGAATGGAATTCCTCTGCTGG 1650
DB 1561 GCCATGAATGCCGAGCCTTCAGATGCCAAGAGGAAAGGAATGGAATTCCTCTGCTGG 1620
QY 1651 AGCCTCCAAAAGAAACAGAGCCTGCCACGCTTGACTTGAGGCCCATTGAAACTGATCTT 1710

DB 1621 AGCCTCCAAAAGAAACAGAGCCTGCCCGCTTGACTTGAGCCCATTGAAACTGATCTT 1680
QY 1711 GAGCTCTGCTGCCCTCCGAATTCAGAGAGATAAATTTGTGTTTAAATGAAAAAAA 1770
DB 1681 GAGCTCTGCTGCCCTCCGAATTCAGAGAGATAAATTTGTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAGAAAAA 1786
DB 1741 AAAAAAAGAAAAA 1756
RESULT 10
US-10-218-849-39
; Sequence 39, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-849-39

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAGCTGGAGTCTGTAGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 91
DB 1 ACCAGCAGAGCTGGAGTCTGTAGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 60
QY 92 GGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACCTGCTCTCTCTTGGCTC 151
DB 61 GGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACCTGCTCTCTCTTGGCTC 120
QY 152 TCAGGCTACTCATTTGCCACTCAAAATCACCGGTCCAAACACAGTGAATGGCTTGAAGCGG 211
DB 121 TCAGGCTACTCATTTGCCACTCAAAATCACCGGTCCAAACACAGTGAATGGCTTGAAGCGG 180
QY 212 GGCTCTTTGACCGTGCAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGGTG 271
DB 181 GGCTCTTTGACCGTGCAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGGTG 240
QY 272 TGTGAGAGGACTATTTGGCGTGAATGCAAGATCTTGTAAACACAGTGGGTTCAGAGCAG 331
DB 241 TGTGAGAGGACTATTTGGCGTGAATGCAAGATCTTGTAAACACAGTGGGTTCAGAGCAG 300
QY 332 GAGGTGAAGAGGAGCGGCTGTCATCAAGACAAATCAGAAACCCGACGTTTCACTGTG 391
DB 301 GAGGTGAAGAGGAGCGGCTGTCATCAAGACAAATCAGAAACCCGACGTTTCACTGTG 360
QY 392 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTGTTGGAAATGAGAAACT 451
DB 361 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTGTTGGAAATGAGAAACT 420

QY 452 GGAATGACCTTGGGTGACAGTTCAGTGAACATTGACCCAGCACCAGTCAACCAAGAA 511
Db 421 GGAATGACCTTGGGTGACAGTTCAGTGAACATTGACCCAGCACCAGTCAACCAAGAA 480
QY 512 GAACTAGCAGCTCCCAACTCTGACCGGCCCACTTGGACAACAGGCAACAGTCTCTG 571
Db 481 GAACTAGCAGCTCCCAACTCTGACCGGCCCACTTGGACAACAGGCAACAGTCTCTG 540
QY 572 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKYGTGTTTGGTGGCCGCC 631
Db 541 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAACATATTKYGTGTTTGGTGGCCGCC 600
QY 632 TCACTCTTGGCTGGAGGATGATGAAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 691
Db 601 TCACTCTTGGCTGGAGGATGATGAAGTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 692 CAGGTACTGACGCCCTTGGAGGCGGACCTTGTCTATGAGACCTGACACCTGAGCTGGCC 751
Db 661 CAGGTACTGACGCCCTTGGAGGCGGACCTTGTCTATGAGACCTGACACCTGAGCTGGCC 720
QY 752 GGAACCTCCCGGAAGGTCACAGAGCTTTCCTCTGCCAGGTTTGACACAGGTGGA 811
Db 721 GGAACCTCCCGGAAGGTCACAGAGCTTTCCTCTGCCAGGTTTGACACAGGTGGA 780
QY 812 GTGGAATATGTCACCATGGCTTCTTCCGGAAGGAGACATTTCTATGATCTCTGACC 871
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Db 841 TTGGGTCTGAGATCAGGAACCGAAGCTTCTGCAACATGAGGCGGCTCAGTACCAATCT 900
QY 932 CCGGGCAGGGGCTGAGGAGGCGGACGAGATACAGACCATCAGAGGCGGCTTACGCTGCA 991
Db 901 CCGGGCAGGGGCTGAGGAGGCGGACGAGATACAGACCATCAGAGGCGGCTTACGCTGCA 960
QY 992 CTCAGGCTCTCTTGGACCCAGGCTGTGAGACACTCTGCTCATCGACCTGCTGC 1051
Db 961 CTCAGGCTCTCTTGGACCCAGGCTGTGAGACACTCTGCTCATCGACCTGCTGC 1020
QY 1052 CCCCTGCTCCCTCATCAGACCAACCCGGGAGCTGCTGCTGATCAGCCAGCA 1111
Db 1021 CCCCTGCTCCCTCATCAGACCAACCCGGGAGCTGCTGCTGATCAGCCAGCA 1080
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Db 1081 TTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCCAAGTCTCAGGGGCTTCTAGGAGTTGGG 1140
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Db 1141 TTTTCTAAACCTCCCTCTCTCTACATAGTTGAGAGGGGCTAGGATATGCTCTGG 1200
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Db 1201 GGCTTTATGGAATGATGAAGATGATAAGAGAAATGTTATCATTTATCATGAAG 1260
QY 1291 TACCATTTACATAACATGAACCTTTATTTATTTGCTTACCAATGTTATGGCTGAAT 1350
Db 1261 TACCATTTACATAACATGAACCTTTATTTATTTGCTTACCAATGTTATGGCTGAAT 1320
QY 1351 AATGGCCCCCAAGATATCTGCTCCTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
Db 1321 AATGGCCCCCAAGATATCTGCTCCTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1380
QY 1411 GCAGAAAGGAGCAGTGCAGATGTATGTAAGTAAAGGACTTTGAGATAGAGAGTTATCT 1470
Db 1381 GCAGAAAGGAGCAGTGCAGATGTATGTAAGTAAAGGACTTTGAGATAGAGAGTTATCT 1440
QY 1471 TGCTGATTCAGGTGGGCCCCAAATATACCAAGAGGCTCCTCATAAGAGAGGCCAGAA 1530
Db 1441 TGCTGATTCAGGTGGGCCCCAAATATACCAAGAGGCTCCTCATAAGAGAGGCCAGAA 1500
QY 1531 GCTCAAGAGGTAGAGACAAAGTGTATGGAAGTGGACCTGGGTGTGACCTGAGCAGG 1590

Db 1501 GGTCAAGAGGTAGAGACAAAGTGTATGATGGAAGTGCACGTGGGTGTGACCTGAGCAGG 1560
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Db 1561 GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGGAAGATGGATTCCCTGCTGG 1620
QY 1651 AGCTCCAAAGAAACACAGCCCTGCCACGCTTGAATTTGAGCCCATTTGAACTGATCTT 1710
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QY 1711 GAGCTCTGGCTCCAGAAATTCAGAGGAGATAAATTTGTGTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCTGGCTCCAGAAATTCAGAGGAGATAAATTTGTGTGTTTAAATGAAAAAAA 1740
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Db 1741 AAAAAAIAAAAAAAAA 1756

RESULT 11
US-10-227-873-39
; Sequence 39, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR FILING DATE: 1999-12-07

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3530PIC78
;; CURRENT APPLICATION NUMBER: US/10/227,883
;; CURRENT FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
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RESULT 13
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 ; Sequence 39, Application US/10219076
 ; Publication No. US20030078379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C62
 ; CURRENT APPLICATION NUMBER: US/10/219,076
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 39
 ; LENGTH: 1837
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-219-076-39

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 QY 32 ACCAGCAGAGGCTGGGAGTCTAGTTGTTCTCTGCTGCCAGGCTCCACTGAGGGAAC 91

Db 1 ACCAGCAGAGGCTGGGAGTCTAGTTGTTCTCTGCTGCCAGGCTCCACTGAGGGAAC 60
 QY 92 GGGGACCTGCTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTTCTTGGCTC 151
 Db 61 GGGGACCTGCTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTTCTTGGCTC 120
 QY 152 TCAGGCTACTCTCATTTGCCACTCAAAATCACCGGTCCAAACAAAGTGAATGGGTGGAGGG 211
 Db 121 TCAGGCTACTCTCATTTGCCACTCAAAATCACCGGTCCAAACAAAGTGAATGGGTGGAGGG 180
 QY 212 GGTCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 271
 Db 181 GGTCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 240
 QY 272 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACCAAGTGGGTGAGAGCAG 331
 Db 241 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACCAAGTGGGTGAGAGCAG 300
 QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACCTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACCTTCACTGTG 360
 QY 392 ACCATGGAGGATCTCATGAAACTGATCTGACACTTACTGCTGGAATTCAGAAAAACT 451
 Db 361 ACCATGGAGGATCTCATGAAACTGATCTGACACTTACTGCTGGAATTCAGAAAAACT 420
 QY 452 GGAATAGACCTTTGGGGTCAACAGTTCAGTGAACCATTGACCCAGCACCACTGACCCAGAA 511
 Db 421 GGAATAGACCTTTGGGGTCAACAGTTCAGTGAACCATTGACCCAGCACCACTGACCCAGAA 480
 QY 512 GAACTAGAGCTCCCAACTCTGACCGGCACACCTTGGAGACAGGCAAGGCTCTG 571
 Db 481 GAACTAGAGCTCCCAACTCTGACCGGCACACCTTGGAGACAGGCAAGGCTCTG 540
 QY 572 AAGCTCAGTGTCTCTGCTCCCTCATCTTCAACATATTTKTYGTGCTTTTGGTGGCGGCC 631
 Db 541 AAGCTCAGTGTCTCTGCTCCCTCATCTTCAACATATTTGCTGCTTTTGGTGGCGGCC 600
 QY 632 TCACCTTTGGCTTGAGGATGATGAAGTACAGAGAAAGAGCGGGGATGTCCTCCAGAG 691
 Db 601 TCACCTTTGGCTTGAGGATGATGAAGTACAGAGAAAGAGCGGGGATGTCCTCCAGAG 660
 QY 692 CAGGTACTGCGAGCCCTGGAGGGGACCTCTGCTATGACAGACCTGACCTCAGCTGCGCC 751
 Db 661 CAGGTACTGCGAGCCCTGGAGGGGACCTCTGCTATGACAGACCTGACCTCAGCTGCGCC 720
 QY 752 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCCAGGTTTACAGGTTGAA 811
 Db 721 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCCAGGTTTACAGGTTGAA 780
 QY 812 GTGGAATATGTCACCATGCTTCTTCCGAGGAGGACATTCCTATGCACTCTGACC 871
 Db 781 GTGGAATATGTCACCATGCTTCTTCCGAGGAGGACATTCCTATGCACTCTGACC 840
 QY 872 TTGGGTGCTGAGGATCAGGAACCGACCTTACTGCAACATGCGGCCAMCTCAGTAGCCACTY 931
 Db 841 TTGGGTGCTGAGGATCAGGAACCGACCTTACTGCAACATGCGGCCAMCTCAGTAGCCACTY 900
 QY 932 CCGGACAGGGCCCTGAGGAGCCCAAGAAATACAGACCATCAGAGGCTTACCTGCA 991
 Db 901 CCGGACAGGGCCCTGAGGAGCCCAAGAAATACAGACCATCAGAGGCTTACCTGCA 960
 QY 992 CTCAGGCTCTTCTTGGACCCAGGCTGTGAGACACTCTCTGCTCATGACGCTGTC 1051
 Db 961 CTCAGGCTCTTCTTGGACCCAGGCTGTGAGACACTCTCTGCTCATGACGCTGTC 1020
 QY 1052 CCCCTGCTCCCTCATCAGGACCAACCCGGGGAATGTTGCTCTGCTGATCAGCAGCA 1111
 Db 1021 CCCCTGCTCCCTCATCAGGACCAACCCGGGGAATGTTGCTCTGCTGATCAGCAGCA 1080
 QY 1112 TTGGCCCTTAGCTCTGGGTTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGAGTGGGG 1171

Db	1081	TTGCCCCAGCTCTGGGTTGGGCTTGGGGCCCAAGTCTCAGGGGGCTTCTAGGAGTTGGG	1140	/	PRIOR FILING DATE: 1997-10-17
QY	1172	TTTTCTTAAGCTCCCTCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG	1230	/	PRIOR APPLICATION NUMBER: 60/063549
Db	1141	TTTTCTTAAGCTCCCTCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG	1200	/	PRIOR FILING DATE: 1997-10-28
QY	1231	GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATTCATGAAG	1290	/	PRIOR APPLICATION NUMBER: 60/064103
Db	1201	GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATTCATGAAG	1260	/	PRIOR FILING DATE: 1997-10-31
QY	1291	TACCATTTATCATTAATCAATGAACCTTTTATTTATTCCTTACACATGTTATGGCTGAAT	1350	/	PRIOR APPLICATION NUMBER: 60/069873
Db	1261	TACCATTTATCATTAATCAATGAACCTTTTATTTATTCCTTACACATGTTATGGCTGAAT	1320	/	PRIOR FILING DATE: 1997-12-17
QY	1351	AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTGTGAGCTGTACTTCTCTGG	1410	/	PRIOR APPLICATION NUMBER: 60/078910
Db	1321	AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTGTGAGCTGTACTTCTCTGG	1380	/	PRIOR FILING DATE: 1998-03-20
QY	1411	GCAGAAAGGACAGTGCAGATGTATGTAACTTAAGGACTTTGAGATGAGAGGTTATCTT	1470	/	PRIOR APPLICATION NUMBER: 60/079294
Db	1381	GCAGAAAGGACAGTGCAGATGTATGTAACTTAAGGACTTTGAGATGAGAGGTTATCTT	1440	/	PRIOR FILING DATE: 1998-03-25
QY	1471	TGCTGATTGAGTGGGCCCCCAATATATCACCAGAGGCTCTCATAGAAAGGCCAGAA	1530	/	PRIOR APPLICATION NUMBER: 60/079656
Db	1441	TGCTGATTGAGTGGGCCCCCAATATATCACCAGAGGCTCTCATAGAAAGGCCAGAA	1500	/	PRIOR FILING DATE: 1998-03-26
QY	1531	GGTCAAGAGGTAGACAAAGTGATGATGAAAGTGAGCGGTGTGACGTGAGCAGGG	1590	/	PRIOR APPLICATION NUMBER: 60/079728
Db	1501	GGTCAAGAGGTAGACAAAGTGATGATGAAAGTGAGCGGTGTGACGTGAGCAGGG	1560	/	PRIOR FILING DATE: 1998-03-27
QY	1591	GCCATGAATCCGAGCGCTTCAGATGCCAGAAAGGAAGGAATGGAATCCCGTGCCTGG	1650	/	PRIOR APPLICATION NUMBER: 60/081819
Db	1561	GCCATGAATCCGAGCGCTTCAGATGCCAGAAAGGAAGGAATGGAATCCCGTGCCTGG	1620	/	PRIOR FILING DATE: 1998-04-15
QY	1651	AGCTCCAAAGAAACACAGCCCTGCCACGCTTGAATTCAGAGCCCATTTGAATCTGATCTT	1710	/	PRIOR FILING DATE: 1998-04-15
Db	1621	AGCTCCAAAGAAACACAGCCCTGCCACGCTTGAATTCAGAGCCCATTTGAATCTGATCTT	1680	/	PRIOR APPLICATION NUMBER: 60/082804
QY	1711	GAGCTCTGGCCTCCAGAAATTCAGAGGAGAAATAATTTGTTGTTTAAATGAAAAAAA	1770	/	PRIOR FILING DATE: 1998-04-22
Db	1681	GAGCTCTGGCCTCCAGAAATTCAGAGGAGAAATAATTTGTTGTTTAAATGAAAAAAA	1740	/	PRIOR APPLICATION NUMBER: 60/084441
QY	1771	AAAAAAAAAAAAAAAAAAAA 1786		/	PRIOR FILING DATE: 1998-05-06
Db	1741	AAAAAAAAAAAAAAAAAAAA 1756		/	PRIOR APPLICATION NUMBER: 60/085323

RESULT 14

US-10-230-434-39

; Sequence 39, Application US/10230434

; Publication No. US20030078380A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C82

; CURRENT APPLICATION NUMBER: US/10/230,434

; CURRENT FILING DATE: 2002-08-28

; PRIOR FILING DATE: 10/119,480

; PRIOR APPLICATION NUMBER: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

;; PRIOR APPLICATION NUMBER: 60/100385
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
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;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAAGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAAC 91
|||
Db 1 ACCAGCAGAAGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAAC 60
QY 92 GGGGACCTGCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTTCTTGGCTC 151
|||
Db 61 GGGGACCTGCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTTCTTGGCTC 120
QY 152 TCAGGCTACTCCATTGCCACTCAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCGG 211
|||
Db 121 TCAGGCTACTCCATTGCCACTCAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCGG 180
QY 212 GGCTCCCTTGACCGTGCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 271
|||
Db 181 GGCTCCCTTGACCGTGCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG 240
QY 272 TGTGAGGAGCTATTGGCGTGACTGCAAGATCCTTGTTAAACCCAGTGGTCAAGACAG 331
|||
Db 241 TGTGAGGAGCTATTGGCGTGACTGCAAGATCCTTGTTAAACCCAGTGGTCAAGACAG 300
QY 332 GAGGTGAAGAGGGACCGGGTGTCCATCAAGCAATCAGAAAAACCGCACGTTCACTGTG 391
|||
Db 301 GAGGTGAAGAGGGACCGGGTGTCCATCAAGCAATCAGAAAAACCGCACGTTCACTGTG 360
QY 392 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGTTGGAATGGAAGAACT 451
|||
Db 361 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGTTGGAATGGAAGAACT 420
QY 452 GGAATGACCTTGGGGTCACAGTTCAAGTGACCACTTGCACCCAGACCCAGTCAACCAAGAA 511
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Db 421 GGAATGACCTTGGGGTCACAGTTCAAGTGACCACTTGCACCCAGACCCAGTCAACCAAGAA 480
QY 512 GAAACTAGCAGCTCCGCACTCTGACCGGCCACACTTGCACCAACAGGCAACAGCTCCTG 571
|||
Db 481 GAAACTAGCAGCTCCGCACTCTGACCGGCCACACTTGCACCAACAGGCAACAGCTCCTG 540
QY 572 AAGCTCAGTGTCTCTGCCCCCTCATCTTCAACATATTKVTGTGCTTTTGGTGGCCGCC 631
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; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090691
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 ; PRIOR APPLICATION NUMBER: 60/166361
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGACGCTGGAGCTGTAGTTGTTCTGTCGAGGCTCCTGAGGGAAC 91

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 16:12:03 ; Search time 4851 Seconds
(without alignments)
11055.963 Million cell updates/sec

Title: US-09-997-131-19
Perfect score: 1796
Sequence: 1 ggaaggaggaagtccaagg.....aaaaaaaaaaggggcgccgc 1796

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	954.6	53.2	1083	BM924147	BM924147 AGENCOURT
2	933.6	52.0	1059	BQ073166	BQ073166 AGENCOURT
3	867.8	48.3	988	BM922663	BM922663 AGENCOURT
4	837.6	46.6	1075	BM923728	BM923728 AGENCOURT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	1	1083 bp	mRNA	linear	EST 12-MAR-2002
BM924147	BM924147	AGENCOURT_6630475	NTM_MGC_116	Homo sapiens	CDNA clone IMAGE:5760369
LOCUS	5', mRNA sequence.				
DEFINITION	5', mRNA sequence.				
ACCESSION	BM924147				
VERSION	BM924147.1	GI:19374526			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1083)				
AUTHORS	NIH-MGC	http://mgi.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12807 row: e column: 10 High quality sequence stop: 705.				

ALIGNMENTS

RESULT	1	1083 bp	mRNA	linear	EST 12-MAR-2002
BM924147	BM924147	AGENCOURT_6630475	NTM_MGC_116	Homo sapiens	CDNA clone IMAGE:5760369
LOCUS	5', mRNA sequence.				
DEFINITION	5', mRNA sequence.				
ACCESSION	BM924147				
VERSION	BM924147.1	GI:19374526			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1083)				
AUTHORS	NIH-MGC	http://mgi.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12807 row: e column: 10 High quality sequence stop: 705.				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	954.6	53.2	1083	BM924147	BM924147 AGENCOURT
2	933.6	52.0	1059	BQ073166	BQ073166 AGENCOURT
3	867.8	48.3	988	BM922663	BM922663 AGENCOURT
4	837.6	46.6	1075	BM923728	BM923728 AGENCOURT

FEATURES
source

Location/Qualifiers
1..1083
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5760369"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 53.2%; Score 954.6; DB 12; Length 1083;
Best Local Similarity 96.6%; Pred. No. 1.2e-155;
Matches 1021; Conservative 6; Mismatches 25; Indels 5; Gaps 5;

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QY 81 CTGAGGGGAAAGGGGACCTGTCTGAAGAGAGATGCCCTCTGCTGACACTCTACCTGTCTCC 140
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 7 CCGGATGAAAGGGGACCTGTCTGAAGAG-AGATGCCCTCTGCTGACACTCTACCTGTCTCC 65
QY 141 TCTTCTGCTCTCAGGCTACTCCATTGCGACTCAAAATCACCGGTCCCAACACAGTGAATG 200
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 66 TCTTCTGCTCTCAGGCTACTCCATTGCGACTCAAAATCACCGGTCCCAACACAGTGAATG 125
QY 201 GCTTGGAGCGGGGTCTCTTGACCGTGCAGTGTGTTACAGATCAGGCTGGAGACCTTACT 260
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 126 GCTTGGAGCGGGGTCTCTTGACCGTGCAGTGTGTTACAGATCAGGCTGGAGACCTTACT 185
QY 261 TGAAGTGTGTGTGTCGAGGAGCTATTGGCGTGTGCTGACATCAAGATCCTTGTAAACACG 320
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 321 GGTGAGAGCAGGAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAAGAAACCGCA 380
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 246 GGTGAGAGCAGGAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAAGAAACCGCA 305
QY 381 CGTTCACTGTGACCATGAGATCTGATGAAACTGATGCTGACACTTACTGTGTGGAA 440
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 306 CGTTCACTGTGACCATGAGGATCTCATGAAACTGATGCTGACACTTACTGTGTGGAA 365
QY 441 TTGAGAAAACCTGGAATGACCTTGGGGTCAAGTTCAGTGCACATTCAGCCAGCACCAG 500
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 366 TTGAGAAAACCTGGAATGACCTTGGGGTCAAGTTCAGTGCACATTCAGCCAGCACCAG 425
QY 501 TCACCCAGAGAAACCTAGAGCTCCGCCAACTCTGACCGGCCACCACTTGGACAAACAGGC 560
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 426 TCACCCAGAGAAACCTAGAGCTCCGCCAACTCTGACCGGCCACCACTTGGACAAACAGGC 485
QY 561 ACAGCTCTTGAAGCTCAGTGTCTCTCTGCCCTCATCTTCAACATATKYTGTCCTTT 620
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 486 ACAGCTCTTGAAGCTCAGTGTCTCTCTGCCCTCATCTTCAACATATKYTGTCCTTT 545
QY 621 TGTGGCGGCTCACTCTTGGCTTGGAGGATGATGAATACAGCAGAAAGCAGCGGGA 680
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 546 TGTGGCGGCTCACTCTTGGCTTGGAGGATGATGAATACAGCAGAAAGCAGCGGGA 605
QY 681 TGTCCCAAGAGCAGGTACTCAGCCCTCGAGGGGACCTCTCTCTATGACAGCTGACCC 740
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 606 TGTCCCAAGAGCAGGTACTCAGCCCTCGAGGGGACCTCTCTCTATGACAGCTGACCC 665
QY 741 TGCAGCTGGCCGGAACCTCCCGCGAAAGAGCTACCAAGCTTTCTCTGCGCCAGGTTG 800
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 666 TGCAGCTGGCCGGAACCTCCCGCGAAAGAGCTACCAAGCTTTCTCTGCGCCAGGTTG 725

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QY 801 ACCAGGTGGAAGTGAATATGTACCATGGCTTCTTCCGGAAGGAGACATTTCTTATG 860
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 726 ACCAGGTGGAAGTGAATATGTACCATGGCTTCTTCCGGAAGGAGACATTTCTTATG 785
QY 861 CATCTCTGACCT-TGGGTCTGAGGATCAGGACCGGACCTACTCTCAACATGGGCCAMCTC 919
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 786 CATCTCTGACCTCGGGGTCTGAGGATCAGGAAAGAGACTACTCTGCAACATGGGCCACCTC 845
QY 920 AGTAGCCATCTCCCGGACAGGGCCCTGAGGAG-CGCACGGAATACAGCACCATCAGC-A 977
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 846 AGTAGCCATCTCCCGGACAGGGCCCTGAGGAGCCCGGGAATACAGCACCATCAGCAA 905
QY 978 GGCCTTAGCTGACACTCCAGGCTCTCTTCTTGACCCCGAGGCTGTGAGCACACTCTCTGCT 1037
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 906 GGCCTTAGCTGACACTCCAGGTTCTTTTGGGACCCAGGCTGTGAGCACACTCTCTGCT 965
QY 1038 CATGACCGCTTGCCCGCTGCTCCCTCATACAGGACCAACCCGGGAGCTGTGTGCTCTGC 1097
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 966 CATGACCGCTTGCCCGCTGCTCCCTCATACAGGACCAACCCCGGAGCTGTGTGCTCTGC 1025
QY 1098 CTG-ATCAGCCAGCATTTGCCCTAGCTCTGGGTGGG 1133
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1026 CCGAATCAGCCAGCATTTGCCCTAGCTCTTGGTTGGG 1062

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RESULT 2
BQ073166
LOCUS BQ073166 1059 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT 6817908 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5757522
5' mRNA sequence.

ACCESSION BQ073166
VERSION BQ073166.1 GI:19902212
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1059)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L2M12799 row: n column: 19
High quality sequence stop: 706.

FEATURES
source

Location/Qualifiers
1..1059
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5757522"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"

/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 52.0%; Score 933.6; DB 13; Length 1059;

QY 410 AAAAAGTGTGACACTTACTGTGTGGAATGAGAACTGGAATGACCTTGGGTC 469
 Db 301 AAAAAGTGTGACACTTACTGTGTGGAATGAGAACTGGAATGACCTTGGGTC 360
 QY 470 ACAGTTCAAGTACCAATGACCAAGCAGCAGTCAACCAAGAGAACTAGCAGCTCCCA 529
 Db 361 ACAGTTCAAGTACCAATGACCAAGCAGCAGTCAACCAAGAGAACTAGCAGCTCCCA 420
 QY 530 ACTCTGACCGGCAACACTTGGACACAGGACAGCTCTCTGAGCTCAGTGTCTCTG 589
 Db 421 ACTCTGACCGGCAACACTTGGACACAGGACAGCTCTCTGAGCTCAGTGTCTCTG 480
 QY 590 CCCCTCATCTTACCACATATTKYTGTTGTTTGTGGCGGCTCCTCTGCTTGGAGG 649
 Db 481 CCCCTCATCTTACCACATATTKYTGTTTGTGGCGGCTCCTCTGCTTGGAGG 540
 QY 650 ATGATGAAGTACCAAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 709
 Db 541 ATGATGAAGTACCAAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 577
 QY 710 GAGGCGACCTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 769
 Db 578 GAGGCGACCTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 637
 QY 770 GTACCAAGAGTCTCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 829
 Db 638 GTACCAAGAGTCTCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 697
 QY 830 GCTTCTTGGCGGAGGACATTTCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGT 889
 Db 638 GCTTCTTGGCGGAGGACATTTCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGT 757
 QY 890 GAACCGACCTACTGCAATGGGCGACCTCAGTAGCCACCTTCCCGGAGGAGTGTGCGGAGT 948
 Db 758 GAACCGACCTACTGCAATGGGCGACCTCAGTAGCCACCTTCCCGGAGGAGTGTGCGGAGT 817
 QY 949 GGAGGCGGAGGAGTACAGCAGCAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 1008
 Db 818 GGAGGCGGAGGAGTACAGCAGCAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 877
 QY 1009 GACCCGAGGCTGTGAGCAGCTTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGT 1065
 Db 878 GACCCGAGGCTGTGAGCAGCTTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGT 937
 QY 1066 ATCAGGACCAACCGGGG 1083
 Db 938 ATCAGGACCAACCGGGG 955

RESULT 4
 BM923728
 LOCUS 1075 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6623860 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5759451
 5', mRNA sequence.
 ACCESSION BM923728
 VERSION BM923728.1 GI:19374107
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1075)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12804 row: 0 column: 04
 High quality sequence stop: 726.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5759451"
 /lab_host="DH103"
 /clone_lib="NIH MGC 116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pMW-SPORE6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 46.6%; Score 837.6; DB 12; Length 1075;
 Best Local Similarity 95.7%; Pred. No. 2.3e-135;
 Matches 890; Conservative 3; Mismatches 32; Indels 5; Gaps 3;
 QY 646 GAGGATGATGAAGTACCAAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 705
 Db 9 GGGATTGATGAAGTACCAAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 65
 QY 706 CTGAGGCGGAGCTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 765
 Db 66 CTGAGGCGGAGCTCTGCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 125
 QY 766 AAAGCTTACCAAGTGTGCTTCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 825
 Db 126 AAAGCTTACCAAGTGTGCTTCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 185
 QY 826 CATGCTTCTTGGCGGAGGACATTTCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 885
 Db 186 CATGCTTCTTGGCGGAGGACATTTCTATGACAGCTGACCTGAGCTGCGGAGTGTGCGGAGTGTGCGGAGT 245
 QY 886 TCAGGACCGACCTACTGCAATGGGCGACCTCAGTAGCCACCTTCCCGGAGGAGTGTGCGGAGTGTGCGGAGT 945
 Db 246 TCAGGACCGACCTACTGCAATGGGCGACCTCAGTAGCCACCTTCCCGGAGGAGTGTGCGGAGTGTGCGGAGT 305
 QY 946 TGAGGAGCGGAGTACAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 1005
 Db 306 TGAGGAGCGGAGTACAGCAGCAGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 365
 QY 1006 TTGAGACCGGAGTGTGAGCAGCTCTGCTGCTATGACAGCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 1065
 Db 366 TTGAGACCGGAGTGTGAGCAGCTCTGCTGCTATGACAGCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 425
 QY 1066 ATCAGGACCAACCGGAGTGTGCTTCTGCTATGACAGCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 1125
 Db 426 ATCAGGACCAACCGGAGTGTGCTTCTGCTATGACAGCTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGT 485
 QY 1126 GGGTGGGCTTGGGCGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 1185
 Db 486 GGGTGGGCTTGGGCGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 545
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QY 1305 TACAATGAACCTTTATTATTGCTTACCAATGTTATGGGTGAATTAATGCCCCCAAG 1364
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QY 1365 ATATCTGTGCTCTAATCTCTCAGAACTTGTGACTGTTACTTCTTCTGGCAGAAAGGACAG 1424
Db 726 ATATCTGTGCTCTAATCTCTCAGAACTTGTGACTGTTACTTCTTCTGGCAGAAAGGACAG 795
QY 1425 TCGAGATGATGATTAAGTAAAGACCTTTCAGATAGAGAGTTATCTTCTGATTCAGGTG 1484
Db 786 TCGAAATGATGATTAAGTAAAGACCTTTCAGATAGAGAGTTATCTTCTGATTCAGGTG 845
QY 1485 GGCACCAATATACACAAAGGCTCTCAT - AAGAAAGAGGCCAGAGAGTCAAAAGAGGTA 1543
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RESULT 5
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DEFINITION 60364005F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213257 5',
mRNA Sequence.
ACCESSION BI911496
VERSION BI911496.1 GI:16175248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1535 row: i column: 02
High quality sequence stop: 875.
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/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(deprecated); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 43.3%; Score 777.6; DB 12; Length 881;
Best Local Similarity 96.1%; Pred. No. 6.2e-125;
Matches 844; Conservative 6; Mismatches 20; Indels 8; Gaps 5;
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Db 5 GGAAAGGGGACCTGTCTGAGAGAGAGATGCCCTGCTGACACTCTACCTGCTCTCTTCT 64
QY 147 GGCTCTCAGGCTACTCCATTGCCACTCAATACCGGTCCAAACAAACAGTGAATGGCTTGG 206
Db 65 GGCTCTCAGGCTACTCCATTGCCACTCAATACCGGTCCAAACAAACAGTGAATGGCTTGG 124
QY 207 AGCGGGGCTCTTTCACCGTGCAGTGTGTTCAGATCAGGCTGGGAGACCTTCTTGAAGT 266
Db 125 AGCGGGGCTCTTTCACCGTGCAGTGTGTTCAGATCAGGCTGGGAGACCTTCTTGAAGT 184
QY 267 GGTGTGTTCAGAGGAGCTATTGCGGTGACTGCAAGATCCTTGTAAACACAGTGGGTCAG 326
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QY 327 AGCAGGAGGTGAAGAGGAGCCGGGTGTCATCAAGGCAATCAAGAAACCGCAGCGTTCA 386
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Db 365 AAATCTGGAATGACTTGGGTTCAGGTCAAGTGCACCTTGAAGTCCACGACACAGTCAACC 424
QY 507 AAGAAAGAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGCAAGC 566
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QY 567 TCCTGAAGCTCAGTGTCTCTGCTGCTCCCTCATCTTTCACCATATTKYGTGCTTTTGGTGG 626
Db 485 TCCTGAAGCTCAGTGTCTCTGCTGCTCCCTCATCTTTCACCATATTKYGTGCTTTTGGTGG 544
QY 627 CGGCTCTACTCTTGGCTGGAGGATGATGAGTACAGGAGAGAGAGAGCGGCGGATGTC 686
Db 545 CGGCTCTACTCTTGGCTGGAGGATGATGAGTACAGGAGAGAGAGAGCGGCGGATGTC 604
QY 687 CAGAG-CAGGTACTGACGCCCTTGGAGGCGAAGCTTGTCTATGCAGACCTTGAACCTGTCAG 745
Db 605 CAGAGNCAGGTACTGACGCCCTTGGAGGCGAAGCTTGTCTATGCAGACCTTGAACCTGTCAG 664
QY 746 CTGGCCGGAACCTCCCGCGA-AGGCTACACAGAGCTTTCCTCTGCCAGGTTGACCA 804
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QY 805 GGTGGAAGTGAATATGTACCAATGCTTCTT--GCCGAAGGAGGACA--TTTCCTATG 860
Db 725 GGTGGAAGTGAATATGTACCAATGCTTCTT--GCCGAAGGAGGACAATTTCTTATG 784
QY 861 CATCTCTGACCTTGGGTGCTGAGGATCAGGAACCGACCTTCTGCAACATGGGCGCMCTCA 920
Db 785 CATCTCTGACCTTGGGTGCTGAGGATCAGGAACCGACCTTCTGCAACATGGGCGCMCTCA 844
QY 921 GTAGCCAMCTYCCCGGAGGCGGCTTGGAGGAGGCCAG 958
Db 845 GTAGCCAC--TCCCGGAGGCGGCTTGGAGGAGGCCAG 880

RESULT 6
CA307972/c
LOCUS 737 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-F71-bib-a-02-0-UI-s1 NCI CGAP_F71 Homo sapiens cDNA clone
UI-H-F71-bib-a-02-0-UI 3', mRNA sequence.
ACCESSION CA307972
VERSION CA307972.1 GI:24471026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 737)
REFERENCE

```

AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
TITLE	Tumor Gene Index	
	Unpublished (1997)	
JOURNAL	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-remail.nih.gov	
COMMENT	Tissue Procurement: Dr. Gary W. Hunninghake, U of I	
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	Clone Distribution: Clone distribution information can be obtained	
	from Dr. M. Bento Soares, bento-soares@uiowa.edu	
	The following repetitive elements were found in this cDNA	
	sequence: 17-452, >MLTID#LTR/MaLR (matched complement)	
	Seq primer: M13 FORWARD	
FEATURES	POLYA=Yes.	
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	/lab_host="DH10B (Life Technologies)"	
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	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a	
	modified polylinker; Site_1: EcoR I; Site_2: Not I;	
	NCI CGAP Ftl is a normalized cDNA library constructed from	
	a pool of 81 RNA samples from Alveolar Macrophages	
	challenged with different treatments. The library was	
	normalized according to Bonaldo, Lennon and Soares, Genome	
	Research, 6:791-806, 1996. First strand cDNA synthesis was	
	primed with an oligo-dT primer containing a Not I site.	
	Double stranded cDNA was ligated to an EcoR I adaptor,	
	digested with Not I, and cloned directionally into	
	pT73-Pac vector. The oligonucleotide used to prime the	
	synthesis of first-strand cDNA contains a library tag	
	sequence that is located between the Not I site and the	
	(dT)18 tail. The sequence tag for this library is	
	GGCATGCGG. The tissue was provided by Dr. Gary W.	
	Hunninghake of the University of Iowa.	
	TAG TISSUE=Human Lung Aveolar Macrophage	
	TAG LIB=UI-H-Ftl	
	TAG_SEQ=GGCCATGCGG"	
ORIGIN	Query Match 39.8%; Score 715; DB 14; Length 737;	
	Best Local Similarity 99.0%; Pred. No. 4.6e-114;	
	Matches 729; Conservative 0; Mismatches 6; Indels 1; Gaps 1;	
	Qy 1052 CCCCTGCTCCCTCATCAGACCAACCCGGGAGTGGTCTCTGCTGATCAGCCAGCA 1111	
	Db 737 CCCCTGCTCCCTCATCAGACCAACCCGGGAGTGGTCTCTGCTGATCAGCCAGCA 678	
	Qy 1112 TTGCCCTAGCTCTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 1171	
	Db 677 TTGCCCTAGCTCTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 618	
	Qy 1172 TTTTCTAAAGTCCCTCCCTCT-CTACATAGTTGAGGAGGGGCTAGGGATAGCTCTGG 1230	
	Db 617 TTTTCTAAAGTCCCTCCCTCTCGACATAGTTGAGGAGGGGCTAGGGATAGCTCTGG 558	
	Qy 1231 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTATCATGAAG 1290	
	Db 557 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTATCATGAAG 498	
	Qy 1291 TACCATTCATATACAAAGACCTTTATTTGCTTACCAATGTTATGGCTGAAT 1350	
	Db 497 TACCATTCATATACAAAGACCTTTATTTATGCTTACCAATGTTATGGCTGAAT 438	
	Qy 1351 AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTTGTAAGTCTGCTCTG 1410	
	Db 437 AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTTGTAAGTCTGCTCTG 378	
	Qy 1411 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470	
	Db 377 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 318	
	Qy 1471 TGCTGATTCAGGTGGGCCCAAAATATCACCACAAAGGTCCTCATAGAAAGAGGCGCAGAA 1530	
	Db 317 TGCTGATTCAGGTGGGCCCAAAATATCACCACAAAGGTCCTCATAGAAAGAGGCGCAGAA 258	
	Qy 1531 GGTCAAGAGGTAGACACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1590	
	Db 257 GGTCAAGAGGTAGACACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 198	
	Qy 1591 GCCATGAATGCCGACGCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCCCTCGG 1650	
	Db 197 GCCATGAATGCCGACGCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCCCTCGG 138	
	Qy 1651 AGCTTCAAAAGAAACAGCCCTCCGACGCTTCGATGATGATGATGATGATGATGATGATGAT 1710	
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	Qy 1711 GAGCTCTGCGCTCCAGAAATTCAGAGGAATAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1770	
	Db 77 GAGCTCTGCGCTCCAGAAATTCAGAGGAATAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 18	
	Qy 1771 AAAAAAATAAAAAA 1786	
	Db 17 AAAAAAATAAAAAA 2	
RESULT 7	CD368538 731 bp mRNA linear EST 29-MAY-2003	
	UI-H-Ftl-bjw-p-15-0-UI.s1 NCI CGAP Ftl Homo sapiens cDNA clone	
LOCUS	UI-H-Ftl-bjw-p-15-0-UI 3', mRNA sequence.	
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ACCESSION	CD368538.1 GI:31152628	
	EST.	
KEYWORDS	Homo sapiens (human)	
	ORGANISM	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1. (bases 1 to 731)	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
JOURNAL	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
COMMENT	Email: cgapbs-remail.nih.gov	
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I	
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	Clone Distribution: Distribution information can be found at	
	http://genome.uiowa.edu/distribution/cgap.html	
	The following repetitive elements were found in this cDNA	
	sequence: 24-445, >MLTID#LTR/MaLR (matched complement)	
	Seq primer: M13 FORWARD	
	POLYA=Yes.	
FEATURES	Location/Qualifiers	
	1..731	
source	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="UI-H-Ftl-bjw-p-15-0-UI"	
	/tissue_type="Aveolar Macrophage"	
	/dev_stage="Adult"	
	/lab_host="DH10B (Life Technologies)"	
	/clone_lib="NCI CGAP Ftl"	
	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a	
	modified polylinker; Site_1: EcoR I; Site_2: Not I;	
	NCI CGAP Ftl is a normalized cDNA library constructed from	
	a pool of 81 RNA samples from Alveolar Macrophages	
	challenged with different treatments. The library was	
	normalized according to Bonaldo, Lennon and Soares, Genome	
	Research, 6:791-806, 1996. First strand cDNA synthesis was	
	primed with an oligo-dT primer containing a Not I site.	
	Double stranded cDNA was ligated to an EcoR I adaptor,	
	digested with Not I, and cloned directionally into	
	pT73-Pac vector. The oligonucleotide used to prime the	
	synthesis of first-strand cDNA contains a library tag	
	sequence that is located between the Not I site and the	
	(dT)18 tail. The sequence tag for this library is	
	GGCATGCGG. The tissue was provided by Dr. Gary W.	
	Hunninghake of the University of Iowa.	
	TAG TISSUE=Human Lung Aveolar Macrophage	
	TAG LIB=UI-H-Ftl	
	TAG_SEQ=GGCCATGCGG"	
	Query Match 39.8%; Score 715; DB 14; Length 737;	
	Best Local Similarity 99.0%; Pred. No. 4.6e-114;	
	Matches 729; Conservative 0; Mismatches 6; Indels 1; Gaps 1;	
Qy	1052 CCCCTGCTCCCTCATCAGACCAACCCGGGAGTGGTCTCTGCTGATCAGCCAGCA 1111	
	Db 737 CCCCTGCTCCCTCATCAGACCAACCCGGGAGTGGTCTCTGCTGATCAGCCAGCA 678	
Qy	1112 TTGCCCTAGCTCTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 1171	
	Db 677 TTGCCCTAGCTCTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 618	
Qy	1172 TTTTCTAAAGTCCCTCCCTCT-CTACATAGTTGAGGAGGGGCTAGGGATAGCTCTGG 1230	
	Db 617 TTTTCTAAAGTCCCTCCCTCTCGACATAGTTGAGGAGGGGCTAGGGATAGCTCTGG 558	
Qy	1231 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTATCATGAAG 1290	
	Db 557 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTATCATGAAG 498	
Qy	1291 TACCATTCATATACAAAGACCTTTATTTGCTTACCAATGTTATGGCTGAAT 1350	
	Db 497 TACCATTCATATACAAAGACCTTTATTTATGCTTACCAATGTTATGGCTGAAT 438	
Qy	1351 AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTTGTAAGTCTGCTCTG 1410	
	Db 437 AATGGCCCCCAAGATATCTGTCTCTTAATCTCAGAACTTGTAAGTCTGCTCTG 378	
Qy	1411 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470	
	Db 377 GCAGAAAGGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 318	
Qy	1471 TGCTGATTCAGGTGGGCCCAAAATATCACCACAAAGGTCCTCATAGAAAGAGGCGCAGAA 1530	
	Db 317 TGCTGATTCAGGTGGGCCCAAAATATCACCACAAAGGTCCTCATAGAAAGAGGCGCAGAA 258	
Qy	1531 GGTCAAGAGGTAGACACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1590	
	Db 257 GGTCAAGAGGTAGACACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 198	
Qy	1591 GCCATGAATGCCGACGCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCCCTCGG 1650	
	Db 197 GCCATGAATGCCGACGCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCCCTCGG 138	
Qy	1651 AGCTTCAAAAGAAACAGCCCTCCGACGCTTCGATGATGATGATGATGATGATGATGATGAT 1710	
	Db 137 AGCTTCAAAAGAAACAGCCCTCCGACGCTTCGATGATGATGATGATGATGATGATGATGAT 78	
Qy	1711 GAGCTCTGCGCTCCAGAAATTCAGAGGAATAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1770	
	Db 77 GAGCTCTGCGCTCCAGAAATTCAGAGGAATAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 18	
Qy	1771 AAAAAAATAAAAAA 1786	
	Db 17 AAAAAAATAAAAAA 2	

NCI CGAP Ftl is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UT-H-F11
TAG_SEQ=GCCCATGCGG"

ORIGIN

Query Match 39.8%; Score 714.8; DB 14; Length 731;
Best Local Similarity 99.5%; Pred. No. 5e-114;
Matches 727; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1051 CCCCCTGCTCCCTCATCAGGACCAACCCGGGACTGGTCCCTGCTGATCAGCCAGC 1110
Db 731 CCCCCTGCTCCCTCATCAGGACCAACCCGGGACTGGTCCCTGCTGATCAGCCAGC 672
Qy 1111 ATTGCCCTAGCTCTGGGTTGGGCTTGGGCCAAGTCTCAGGGGGCTTCTAGAGTTGGG 1170
Db 671 AGTGCCCTAGCTCTGGGTTGGGCTTGGGCCAAGTCTCAGGGGGCTTCTAGAGTTGGG 612
Qy 1171 GTTTTCTAAGCTCCCTCCTCT-CTACATAGTTGAGGAGGGGCTAGGGATGCTCTG 1229
Db 611 GTTTTCTAAGCTCCCTCCTCTCTCATATAGTTGAGGAGGGGCTAGGGATGCTCTG 552
Qy 1230 GGGCTTTTCATGGGAAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAA 1289
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Qy 1290 GTACCATATCATTAATCAATGAACCTTTATTTATGCTTACCATGATGTTATGGCTGAA 1349
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Qy 1470 TTGCTGATTCAGTGGGCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGA 1529
Db 311 TTGCTGATTCAGTGGGCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGA 252
Qy 1530 AGGTCAAGAGGTAGAGCAAAAGTATGATGGAAGTGGACGTGGGTGTGACGTGAGCAGG 1589
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Db 191 GGCATGAATGCGCAGCCTTCAGATGCCAGAAAGGGAAGGAATGATTCCTCCCTGCTG 132
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Db 131 GAGCTCCCAAGAAACAGCCCTGCCACGCCCTTGACTTCAGGCCCTTGAACCTGATCT 72
Qy 1710 TGAGCTCTGGCCTCCAGAAATTCAGGAGATAAATTTGTGTTTAAATGAAAAAAA 1769
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Db 11 AAAAAA 1

RESULT 8

BI818421
LOCUS
DEFINITION

ACCESSION

BI818421
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

BI818421 759 bp mRNA linear EST 04-OCT-2001
603033889F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173919 5',
mRNA sequence.
BI818421
BI818421.1 GI:15929260
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9abb-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1433 row: a column: 24
High quality sequence stop: 757.
Location/Qualifiers
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/note="Organ: pooled brain, lung, testis; Vector:
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 38.5%; Score 692.2; DB 12; Length 759;
Best Local Similarity 96.4%; Pred. No. 4.1e-110;
Matches 726; Conservative 3; Mismatches 21; Indels 3; Gaps 2;

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

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D 361 GTGTGGAATTGAGAACTGGAATGACCTTGGGTCACAGTTTCAAGTGACCATGACCC 420
QY 493 AGCAGCAGTCAACCCAGAGAACTAGCAGCTCCCAACTCTGACCGCCACCACTTGGGA 552
D 421 AGCAGCAGTCAACCCAGAGAACTAGCAGCTCCCAACTCTGACCGCCACCACTTGGGA 480
QY 553 CAAAGGCAAGAGCTCTGAGAGCTCAGTGTCTCTGCTGCTTCACTTTCACCATATTKYT 612
D 481 CAAAGGCAAGAGCTCTGAGAGCTCAGTGTCTCTGCTGCTTCACTTTCACCATATTKYT 540
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D 541 GYTGCTTTTGTGGCGGCTCACTCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGC 600
QY 673 AGCCGGAGTGTCCCGAGAGGAGTACTGCA--GCCCTGGAGGCGACCTCTGCTATGCA 730
D 601 AGCCGGAGTGTCCCGAGAGGAGTACTGCAAGAGCCCTGGAGGCGAGTCTTGTCTATGCA 660
QY 731 GACCTGACCTGCA--GCTGGCGGAGACCTCCCGGAGAGCTACACGAGCTTTCCTC 789
D 661 GACCTGACCTGCA--GCTGGCGGAGACCTCCCGGAGAGCTACACGAGCTTTCCTC 720
QY 790 TGCCAGGTTGACCAAGTGGAGTGGATATGT 822
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RESULT 9
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DEFINITION
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  UI-E-EJ0-aim-f-06-0-UI-s1 UI-E-EJ0 Homo sapiens cDNA clone
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ACCESSION
  BM680508
VERSION
  BM680508.1 GI:18990404
KEYWORDS
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SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 699)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  97044477
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  The following repetitive elements were found in this cDNA
  sequence: 17-452, >MLR1D#LTR/MaLR (matched compliment)
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Matches 691; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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D 519 TCTTATCATTTATTCATGAAGTACCATATATCAATAACAATGAACCTTTATTTATGCC 460
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D 399 CTTGTGACTGTTTACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGAC 340
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D 339 TTTGAGATAGAGAGTTTATTTCTGCTGATTCAGTGGGCCCCCAAAATATCACCACAGGT 280
QY 1509 CCTCATAGAAGAGAGCCAGAGGTCAAAAGGTAGAGACAAAGTATGATGGGAAGTGA 1568
D 279 CCTCATAGAAGAGAGCCAGAGGTCAAAAGGTAGAGACAAAGTATGATGGGAAGTGA 220
QY 1569 CTGTGGTGTGACGTAGCAGGGGCCATGATGCGCGAGCTTTCAGATGCCAGAAAGGAA 1628
D 219 CTGTGGTGTGACGTAGCAGGGGCCATGATGCGCGAGCTTTCAGATGCCAGAAAGGAA 160
QY 1629 AGGAATGATTTCCCTGCTGGAGCTCCAAAAGAAACACAGCCCTGCCAGCCCTTGACT 1688
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UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCA; eye anterior segment,
AATGCGCAT; optic nerve, CCAATAGTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTG. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
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DEFINITION		UI-H-FT1-bka-j-15-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone	
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VERSION		CD367917.1	GI:31152007
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		1 (bases 1 to 661)	
AUTHORS		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL		Tumor Gene Index	
COMMENT		Unpublished (1997)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgaps-remail.nih.gov	
		cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
		Clone Distribution: Distribution information can be found at	
		http://genome.uiowa.edu/distribution/cgap.html	
		Seq primer: M13 FORWARD	
POLYA-Yes			
FEATURES		Location/Qualifiers	
source		1..661	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="UI-H-FT1-bka-j-15-0-UI"	
		/tissue_type="Aveolar Macrophage"	
		/dev_stage="adult"	
		/lab_host="DH10B (Life Technologies)"	
		/clone_lib="NCI CGAP FT1"	
		/note="Organ: Lung; Vector: p7T73-Pac (Pharmacia) with a	
		modified polylinker; Site 1: EcoR I; Site 2: Not I;	
		NCI CGAP FT1 is a normalized cDNA library constructed from	
		a pool of 81 RNA samples from Alveolar Macrophages	
		challenged with different treatments. The library was	
		normalized according to Bonaldo, Lennon and Soares, Genome	
		Research, 6:791-806, 1996. First strand cDNA synthesis was	
		primed with an oligo-dT primer containing a Not I site.	
		Double stranded cDNA was ligated to an EcoR I adaptor,	
		digested with Not I, and cloned directionally into the	
		p7T73-pac vector. The oligonucleotide used to prime the	
		synthesis of first-strand cDNA contains a library tag	
		sequence that is located between the Not I site and the	
		(dfr)18 tail. The sequence tag for this library is	
		GGCCATGCGG. The tissue was provided by Dr. Gary W.	
		Hunninghake of the University of Iowa.	
		TAG TISSUE=Human Lung Aveolar Macrophage	
		TAG_LIB=UI-H-FT1	
		TAG_SEQ=GGCCATGCGG"	
ORIGIN			
Query Match		34.5%; Score 620.2; DB 14; Length 661;	
Best Local Similarity		99.1%; Pred. No. 1.3e-97;	
Matches 641; Conservative		3; Mismatches 1; Indels 2; Gaps 2;	
Qy	645	GGAGGATGATGAAGTACAGCAGAGAAAGCAGCCGGGATGTCCCGAGAGACTACTGCAGC	704

661	GGAGGATGATGAAGTACCCAGCAAGAGCGAGGATGTCCCGAGAGAGGACTACTGCAGC	602
705	CCCTGGAGGGGAGCCTCTGCTATGACAGCTGACCTGACCTGCGCGGAACCTCCCGC	764
601	CTTGGAGGGGAGCCTCTGCTATGAGAGCTGACCTGCGAGTGGCGGAAACCTCCCGC	542
765	GAAAGGCTACCAAGAGCTTTCTCTGCCCAAGTTGACCAAGTGGAGTGAATATGTCA	824
541	GAAAGGCTACCAAGAGCTTTCTCTGCCCAAGTTGACCAAGTGGAGTGAATATGTCA	482
825	CCATGGCTTCCTTCCGAGGAGGACATTTCTCTATGATCTCTGACCTTGGGTGCTGAGG	884
481	CAATGGCTTCCTTCCGAGGAGGACATTTCTCTATGATCTCTGACCTTGGGTGCTGAGG	422
885	ATCAGGAAACCGACCTACTGCAACATGCGGCCAMCTCAGTAGCCAMCTVCCCGCAGGGGCC	944
421	ATCAGGAAACCGACCTACTGCAACATGCGGCCAMCTCAGTAGCCAMCTVCCCGCAGGGGCC	362
945	CTGAGGAGCCACCGAATACAGCACCATCAGAGGCTTAGCCTGCATCTCCAGGCTCCTT	1004
361	CTGAGGAGCCACCGAATACAGCACCATCAGAGGCTTAGCCTGCATCTCCAGGCTCCTT	302
005	CTTGGACCCCGAGGCTGTGAGACACTCTCTGCCCTCATCGACCTCTGCCCTGCTCCCT	1064
301	CTTGGACCCCGAGGCTGTGAGCACACTCTCTGCCCTCATCGACCTCTGCCCTGCTCCCT	242
065	CATCAGGACCAACCCGGGAGCTGTGCTCTGCTCTGATCAGCCAGCATTCGCCCTAGCTC	1124
241	CATCAGGACCAACCCGGGAGCTGTGCTCTGCTCTGATCAGCCAGCATTCGCCCTAGCTC	182
125	TGGGTTGGGCTTGGGGCCAACTCTCAGGGGCTTCTAGGAGTTGGGTTTTCTAAACGTC	1184
181	TGGGTTGGGCTTGGGGCCAACTCTCAGGGGCTTCTAGGAGTTGGGTTTTCTAAACGTC	122
185	CCCTCTCT-CTACATAGTTGAGGAGGGGCTTAGGATATGCTCTGGGCTTTC-ATGGG	1242
121	CCCTCTCTCTCTACATAGTTGAGGAGGGGCTTAGGATATGCTCTGGGCTTTCATATGGG	62
1243	AATGATGAGATGATTAATGAGAAAAATGTTATCATTTATTCATGAA	1289
61	AATGATGAGATGATTAATGAGAAAAATGTTATCATTTATTCATGAA	15
AW003259 560 bp mRNA linear EST 08-SEP-1999		
wq64f09.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2476073 3',		
mRNA sequence.		
AW003259		
AW003259.1 GI:5850175		
EST.		
Homo sapiens (human)		
Homo sapiens		
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 560)		
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
Tumor Gene Index		
Unpublished (1997)		
Contact: Robert Strausberg, Ph.D.		
Email: cgaps-remail.nih.gov		
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael		
R. Emmert-Buck, M.D., Ph.D.		
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima		
Bonaldo, Ph.D.		
cDNA Library Arrayed by: Greg Lennon, Ph.D.		
DNA sequencing by: Washington University Genome Sequencing Center		
Clone distribution: NCI-CGAP clone distribution information can be		
found through the I.M.A.G.E. Consortium/LLNL at:		
www.bio.llnl.gov/bbrp/image/image.html		
Seq primer: -40UP from Gibco		

High quality sequence stop: 477.

FEATURES
source

Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2476073"
/tissue type="pooled germ cell tumors"
/lab host="DH10B"
/clone lib="NCI CGAP GC6"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 30.4%; Score 546; DB 9; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-84;
Matches 557; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1207 GAGGGGCTAGGATATCTCTGGGCTTTCATGGGAATGATGAAGATGATATGAGAAA 1266
DB 560 GAGGGGCTAGGATATCTCTGGGCTTTCATGGGAATGATGAAGATGATATGAGAAA 501
QY 1267 AATGTTATCATTTATCATCAAGTACCATATATCATTAATCAATGAACCTTTATTTATG 1326
DB 500 AATGTTATCATTTATCATCAAGTACCATATATCATTAATCAATGAACCTTTATTTATG 441
QY 1327 CTTACCAATGTTATGGCTGAATAATGGCCCCCAAGATATCTGTCTCTTAATCTCCAG 1386
DB 440 CTTACCAATGTTATGGCTGAATAATGGCCCCCAAGATATCTGTCTCTTAATCTCCAG 381
QY 1387 AACTTGTGACTGTTACCTTCTGTGCGAAGGACAGTCAGATGATGTAGTTAAGG 1446
DB 380 AACTTGTGACTGTTACCTTCTGTGCGAAGGACAGTCAGATGATGTAGTTAAGG 321
QY 1447 ACTTGTGATAGAGAGTTATTTCTGTGATTCAGGTGGGCCCAAAATATCACCAAG 1505
DB 320 ACTTGTGATAGAGAGTTATTTCTGTGATTCAGGTGGGCCCAAAATATCACCAAG 261
QY 1506 GGTCTCTATAGAAAGGCGCAGAGTCAAGAGGTAGACAAAGTGTAGTTGAAGT 1565
DB 260 GGTCTCTATAGAAAGGCGCAGAGTCAAGAGGTAGACAAAGTGTAGTTGAAGT 201
QY 1566 GGAGCTGGGTGTGACGTGAGCAGGGGCGCATGAATGCCCGACCTTCAGATGCCAGAAAGG 1625
DB 200 GGAGCTGGGTGTGACGTGAGCAGGGGCGCATGAATGCCCGACCTTCAGATGCCAGAAAGG 141
QY 1626 GAAAGGAATGATTCCTGCTGGAGCTCCAAAGAAACCAAGCCCTGCCACGCTTG 1685
DB 140 GAAAGGAATGATTCCTGCTGGAGCTCCAAAGAAACCAAGCCCTGCCACGCTTG 81
QY 1686 ACTTGAGCCCATTTGAATCTGATCTTGAGCTCTGCTGCTCCAGAAATTCAGAGAAATAAT 1745
DB 80 ACTTGAGCCCATTTGAATCTGATCTTGAGCTCTGCTGCTCCAGAAATTCAGAGAAATAAT 21
QY 1746 TTGTGTTGTTTAAATGA 1763
DB 20 TTGTGTTGTTTAAATGA 3

RESULT 12
CF541209/c
LOCUS
DEFINITION
UI-CF-EC1-adt-g-10-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
ACCESSION
CF541209
VERSION
CF541209.1 GI:34593732

KEYWORDS
SOURCE
ORGANISM

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 568)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
The following repetitive elements were found in this cDNA
sequence: 24-446, >MLTID#LTR/MaLR (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cf.html
The following repetitive elements were found in this cDNA
sequence: 24-446, >MLTID#LTR/MaLR (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Source

Location/Qualifiers
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-adt-g-10-0-UI"
/tissue type="Lung"
/dev stage="Adult and Fetal"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3D-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the idr18 tail. The sequence tag for this library is AAGTGGCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGGCTTAC"

ORIGIN

Query Match 30.3%; Score 544.8; DB 14; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.6e-84;
Matches 557; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1222 ATGCTCTGGGCTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTAT 1281
DB 560 ATGCTCTGGGCTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTAT 501
QY 1282 ATCATGAAGTACCATTTATCATATACAAATGAACCTTTATTTATTTATTTATTTAT 1341
DB 500 ATCATGAAGTACCATTTATCGTAATACAAATGAACCTTTATTTATTTATTTATTTAT 441
QY 1342 GGGCTGATATATGCCCCCAAGATATCTGTGCTCTTAATCTCTCAGAACTTGTGACTGTTA 1401

Db 440 GGCTGTAATATGGCCCCCAAGATATCTGTGTCCTAATCCTCAGAACCTGTGACTGTTA 381
Qy 1402 CTTCTGTGCGCAGAAAGGACAGTGCAGATGTAAGTAAAGGACTTTGAGATAGAGA 1461
Db 380 CTTCTGTGCGCAGAAAGGACAGTGCAGATGTAAGTAAAGGACTTTGAGATAGAGA 321
Qy 1462 GGTATTCTTCTGTGATTCAGTGGGCCCAAAATATCACACAGGCTCTCTCATAGAAAG 1521
Db 320 GGTATTCTTCTGTGATTCAGTGGGCCCAAAATATCACACAGGCTCTCTCATAGAAAG 261
Qy 1522 AGCCAGAAAGGTCAAAGAGTAGAGACAAAGTGAATGATGGAAGTGAAGTGAAGTGAAG 1581
Db 260 AGCCAGAAAGGTCAAAGAGTAGAGACAAAGTGAATGATGGAAGTGAAGTGAAGTGAAG 201
Qy 1582 TGACAGGGCCATGATGCGGAGCTTCAGATGCGAGAAAGGAAAGGATGGATTC 1641
Db 200 TGACAGGGCCATGATGCGGAGCTTCAGATGCGAGAAAGGAAAGGATGGATTC 141
Qy 1642 CTTGCTGTGAGCTTCAAAAGAAACACAGCCCTGCCACGCTTGACTTGAGCCCATTTGAA 1701
Db 140 CTTGCTGTGAGCTTCAAAAGAAACACAGCCCTGCCACGCTTGACTTGAGCCCATTTGAA 81
Qy 1702 ACTGATCTTGTGCTCTGGCT-CCAGAAATGAGGAGATAAATTTGTTGTTTTTAA 1760
Db 80 ACTGATCTTGTGCTCTGGCTCCAGATTCAGAGGAGATAAATTTGTTGTTTTTAA 21
Qy 1761 TGAAGAAAAAAGAAAAA 1780
Db 20 TGAAGAAAAAAGAAAAA 1

RESULT 13
BI906782
LOCUS 595 bp mRNA linear EST 16-OCT-2001
DEFINITION 603064528F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213623 5',
mRNA sequence.
ACCESSION BI906782
VERSION BI906782.1 GI:16169540
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1536 row: h column: 08
High quality sequence stop: 595.
Location/Qualifiers
1. 595
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5213623"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 29.5%; Score 529.2; DB 12; Length 595;
Best Local Similarity 96.7%; Pred. No. 8.1e-82;
Matches 551; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Qy 1217 GGGATATCTCTGGGGCTTCATGGATGATGAGATGATAATGAGAAAAATGTATCA 1276
Db 1 GGGATATCTCTGGGGCTTCATGGATGATGAGATGATAATGAGAAAAATGTATCA 59
Qy 1277 TTATTATCATGAAGTACCATTATCATATAACAATGAACCTTTATTATGCTACCACAT 1336
Db 60 TTATTATCATGAAGTACCATTATCATATAACAATGAACCTTTATTATGCTACCACAT 119
Qy 1337 GTTATGGGCTGAATAATGGCCCCCAAGATATCTGTGCTCTAACTCCTCAGAACTTGTGAC 1396
Db 120 GTTATGGGCTGAATAATGGCCCCCAAGATATCTGTGCTCTAACTCCTCAGAACTTGTGAC 179
Qy 1397 TGTACCTTCTGTGGCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGAT 1456
Db 180 TGTACCTTCTGTGGCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGAT 239
Qy 1457 AGAGAGGTTATTCTTGTGCTGATTCAGTGGGCCCAAAATATCACACAGGCTCTCTATAA 1516
Db 240 AGAGAGGTTATTCTTGTGCTGATTCAGTGGGCCCAAAATATCACACAGGCTCTCTATAA 299
Qy 1517 GAAAGGCGCAGAGGTCAGAGAGGTAGAGACAAAGTGCATGATGGAAGTGCAGCTGGGTG 1576
Db 300 GAAAGGCGCAGAGGTCAGAGAGGTAGAGACAAAGTGCATGATGGAAGTGCAGCTGGGTG 359
Qy 1577 TGACGTGAGCAGGGGCCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGAAATGG 1636
Db 360 TGACGTGAGCAGGGGCCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGAAATGG 419
Qy 1637 ATTCCCTTCTGTGGAGCTTCGAAAGAAACAGCCCTGCCACGCTTGCCTTGGAGCCCA 1696
Db 420 ATTCCCTTCTGTGGAGCTTCGAAAGAAACAGCCCTGCCACGCTTGCCTTGGAGCCCA 479
Qy 1697 TTGAAGTATGATCTTGTGCTCTTGGCTTCCAGAAATTCAGAGGAGAAATAATTTGTGTTT 1756
Db 480 TTGAAGTATGATCTTGTGCTCTTGGCTTCCAGAAATTCAGAGGAGAAATAATTCGTGTTT 539
Qy 1757 TTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 1786
Db 540 AATGAGCCAAAAAAGAAAAAAGAAAAAAGAAAAA 569

RESULT 14
CD695911
LOCUS 564 bp mRNA linear EST 25-JUN-2003
DEFINITION EST12434 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD695911
VERSION CD695911.1 GI:32221917
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 564)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:23:39 ; Search time 121 Seconds

(without alignments)
677.180 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 1499

Sequence: 1 MPRLTYLLFLWLSGVSIAT.....SXLPGRGPPEPEYSTISRP 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1493	99.6	290	4 AAB74712	Aab74712 Human mem
2	1493	99.6	290	5 AAU83611	Aau83611 Human PRO
3	1493	99.6	290	6 ABU80758	Abu80758 Human PRO
4	1493	99.6	290	6 ABO33724	AbO33724 Novel hum
5	1493	99.6	290	6 ABU82067	Abu82067 Novel hum
6	1493	99.6	290	6 ABJ72247	Abj72247 Human PRO
7	1493	99.6	290	6 ABJ72375	Abj72375 Human PRO
8	1493	99.6	290	6 ABO34270	AbO34270 Human sec
9	1493	99.6	290	7 ABJ72077	AbJ72077 Human mem
10	1493	99.6	290	7 ADB83530	AdB83530 Novel hum
11	1493	99.6	290	7 ADB80636	AdB80636 Novel hum
12	1493	99.6	290	7 ADB73177	AdB73177 Novel hum
13	1493	99.6	290	7 ADB78259	AdB78259 Novel hum
14	1493	99.6	290	7 ADB84907	AdB84907 Human PRO
15	1493	99.6	290	7 ADB78013	AdB78013 Novel hum
16	1493	99.6	290	7 ADB87079	AdB87079 Human PRO
17	1493	99.6	290	7 ADB84661	AdB84661 Human PRO
18	1493	99.6	290	7 ADB83776	AdB83776 Novel hum
19	1493	99.6	290	7 ADB72931	AdB72931 Novel hum
20	1493	99.6	290	7 ADC35769	AdC35769 Human PRO
21	1493	99.6	290	7 ADC21759	AdC21759 Human PRO
22	1493	99.6	290	7 ADC49790	AdC49790 Novel hum
23	1493	99.6	290	7 ADC49898	AdC49898 Novel hum
24	1493	99.6	290	7 ADC49506	AdC49506 Novel hum
25	1493	99.6	290	7 ADC47367	AdC47367 Novel hum

ALIGNMENTS

RESULT 1
AAB74712
ID AAB74712 standard; protein; 290 AA.
XX AC AAB74712;
XX DT 12-JUN-2001 (first entry)
XX DE Human membrane associated protein MEMAP-18.
XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
XX KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
XX KW antiatherosclerotic; gene therapy; cell proliferative disorder;
XX KW autoimmune disorder; inflammatory disorder; neurological disorder;
XX KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
XX KW epilepsy; diarrhoea.
XX OS Homo sapiens.
XX PN WO200112662-A2.
XX PD 22-FEB-2001.
XX PP 14-AUG-2000; 2000WO-US022315.
XX PR 17-AUG-1999; 99US-0149641P.
XX PR 09-NOV-1999; 99US-0164203P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughm MR, Lu DAM, Patterson C;
XX WPI; 2001-168860/17.
XX N-PSDB; AAF81758.
PT Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX Claim 1; Page 131-132; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
XX (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
XX antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
XX antiatherosclerotic activities, which can be used in gene therapy
XX MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
XX associated with decreased expression of functional MEMAP and antagonists

26 1493 99.6 290 7 ADC47112 AdC47112 Novel hum
27 1493 99.6 290 7 ADC77987 AdC77987 Novel hum
28 1493 99.6 290 7 ADD05222 AdD05222 Novel hum
29 1493 99.6 290 7 ADC77741 AdC77741 Novel hum
30 1493 99.6 290 7 ADD50704 AdD50704 Novel hum
31 1493 99.6 290 7 ADD50950 AdD50950 Novel hum
32 1493 99.6 290 7 ADD50431 AdD50431 Human PRO
33 1493 99.6 290 7 ADD50185 AdD50185 Human PRO
34 1493 99.6 290 7 ADD51196 AdD51196 Novel hum
35 1493 99.6 290 8 ADC48743 AdC48743 Novel hum
36 1493 99.6 290 8 ADE20914 AdE20914 Novel hum
37 1493 99.6 290 8 ADE05758 AdE05758 Human PRO
38 1493 99.6 290 8 ADD74987 AdD74987 Human PRO
39 1493 99.6 290 8 ADD75733 AdD75733 Novel hum
40 1493 99.6 290 8 AGD84965 AdG84965 Novel hum
41 1493 99.6 290 8 AGD86791 AdG86791 Novel hum
42 1493 99.6 290 8 ADE20668 AdE20668 Novel hum
43 1493 99.6 290 8 ADE38965 AdE38965 Novel hum
44 1493 99.6 290 8 ADE05512 AdE05512 Human PRO
45 1493 99.6 290 8 ADD73497 AdD73497 Human PRO

CC of MEMAP are used to treat a disease or condition associated with
 CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated with
 CC MEMAP
 XX
 SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 4; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 DB 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDQETPCNMGLSSKLPGRPEPTETSTISRP 290
 DB 241 SLPKEDISYASLTGAEDQETPCNMGLSSKLPGRPEPTETSTISRP 290

RESULT 2
 AAU83611
 ID AAU83611 standard; protein; 290 AA.
 XX
 AC AAU83611;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 40.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021066.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220585P.
 PR 25-JUL-2000; 2000US-0220605P.
 PR 25-JUL-2000; 2000US-0220607P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.
 PR 25-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-AUG-2000; 2000US-022425P.
 PR 22-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CX, Wood WI;
 XX
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABK33555.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 PS Claim 11; Fig 40; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumor necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 5; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 DB 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240

Qy 241 SLPKEDISYASLTGAEDEPTTCNMGXLSXLPGRGPPEPTSTSRP 290
Db 241 SLPKEDISYASLTGAEDEPTTCNMGXLSXLPGRGPPEPTSTSRP 290
RESULT 3
ABU80758
AC ABU80758 standard; protein; 290 AA.
XX
XX 23-JUN-2003 (first entry)
XX Human PRO polypeptide #20.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
KW
XX Homo sapiens.
XX US2003036635-A1.
XX 20-FEB-2003.
XX 28-AUG-2002; 2002US-00230163.
XX 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
DR N-PSDB; ACA66860.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 40; 314pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX useful in diagnostic assays for PRO, by detecting its expression in
XX specific cells, tissues or serum, and for affinity purification of PRO
XX from recombinant cell culture or natural sources. ABUS0739-ABUS0860
XX represent the human PRO polypeptides of the invention. Note: The sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipspidentry.html
XX
XX Sequence 290 AA;
Query Match 99.6%; Score 1493; DB 6; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Qy 61 DCKILVKTSGSFOEYKRDVSIKQNKRTFTVMDLTKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSFOEYKRDVSIKQNKRTFTVMDLTKTDADTYWCGIEKTGNDLGVT 120
Qy 121 VQVITDPAPVTQEBTSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAALLAWRM 180

Db 121 VQVITDPAPVTQEBTSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAALLAWRM 180
Qy 181 MKYQKKAAGMSPEQVLQPLEGDLCLYADLTQLAGTSRKAATKLSACVDCVEYVYVMA 240
Db 181 MKYQKKAAGMSPEQVLQPLEGDLCLYADLTQLAGTSRKAATKLSACVDCVEYVYVMA 240
Qy 241 SLPKEDISYASLTGAEDEPTTCNMGXLSXLPGRGPPEPTSTSRP 290
Db 241 SLPKEDISYASLTGAEDEPTTCNMGXLSXLPGRGPPEPTSTSRP 290
RESULT 4
ABO33724
ID ABO33724 standard; protein; 290 AA.
XX
XX ABO33724;
XX 17-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO10111.
XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX Homo sapiens.
OS
XX US2003045687-A1.
XX 06-MAR-2003.
XX 12-AUG-2002; 2002US-00218631.
XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-512315/48.
DR N-PSDB; ACD68612.
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
XX Claim 11; Fig 40; 314pp; English.
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
XX 122 PRO (secreted and transmembrane) polypeptides whose sequences are
XX fully defined in the specification; or (b) any of 122 nucleotide
XX sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
XX specification; or the full length coding sequence of any these 122
XX nucleotide sequences. The PRO polypeptides or polynucleotides are useful
XX as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
XX particularly useful for detecting tumours (e.g. lung tumour, colon
XX tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
XX in a mammal, for stimulating the release of TNF-alpha from human blood,
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells, for stimulating proliferation of pericyte cells, or for modulating
XX normal human dermal fibroblast proliferation. The PRO nucleic acid or
XX polypeptide is also useful for treating tumours or various bone and/or
XX cartilage disorders (e.g. sports injuries or arthritis), or wounds. The

CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 XX

CC Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 6; Length 290;
 Best Local Similarity 99.0%; Pred: No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPELLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQKQRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKQKQRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 DB 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLQPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVYMA 240
 DB 181 MKYQKAAAGMSPEQVLQPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVYMA 240
 QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXKLPGRGPEEPTSTISRP 290
 DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXKLPGRGPEEPTSTISRP 290

RESULT 5

ID ABU82067
 XX ABU82067 standard; protein; 290 AA.
 AC ABU82067;
 XX
 XX
 XX 25-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX
 KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW anglogenetic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 XX US2003088063-A1.
 XX
 XX 08-MAY-2003.
 PD
 XX 12-AUG-2002; 2002US-00219003.
 PF
 XX 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (G5TH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-393229/37.
 DR N-PSDB; ACA68516.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angio-genic disorders in a mammal.
 XX
 PS Claim 11; Fig 40; 314pp; English.

CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angio-genic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 6; Length 290;

Best Local Similarity 99.0%; Pred: No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQKQRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKQKQRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 DB 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLQPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVYMA 240
 DB 181 MKYQKAAAGMSPEQVLQPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVYMA 240
 QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXKLPGRGPEEPTSTISRP 290
 DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXKLPGRGPEEPTSTISRP 290

RESULT 6

ID ABU72247
 XX ABU72247 standard; protein; 290 AA.
 AC ABU72247;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 XX Human PRO10111 protein.
 DE
 DE
 KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX US2003050448-A1.
 XX
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002US-00210414.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.

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PR 09-APR-2002; 2002US-00119480.
XX (GETH ) GENENTECH INC.
PA
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-521818/49.
XX N-PSDB; ABT44245.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX
XX Claim 11; Fig 40; 315pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of human dermal fibroblast cell
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
CC protein of the invention
XX
XX Sequence 290 AA;
SQ
Query Match 99.6%; Score 1493; DB 6; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
Db 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLOPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLOPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTETSTISRP 290
Db 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTETSTISRP 290
RESULT 7
ABJ72375
XX ID ABJ72375 standard; protein; 290 AA.
XX AC
XX ABJ72375;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human PRO10111 protein.
XX
XX PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
XX Homo sapiens.
OS
XX US2003027988-A1.
PN

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XX 06-FEB-2003.
XX
XX 26-AUG-2002; 2002US-00227884.
XX
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-503301/47.
XX N-PSDB; ABT44528.
XX
XX New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
XX Claim 11; Fig 40; 324pp; English.
XX
XX The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC polypeptides in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
XX Sequence 290 AA;
SQ
Query Match 99.6%; Score 1493; DB 6; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
Db 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLOPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLOPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTETSTISRP 290
Db 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTETSTISRP 290
RESULT 8
ABO34270
XX ID ABO34270 standard; protein; 290 AA.
XX AC
XX ABO34270;
XX
XX 19-SEP-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO 10111.
XX
XX Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
XX human dermal fibroblast stimulation; tumour; tissue typing;
KW

```

KW affinity purification.
 OS Homo sapiens.
 XX US2003044934-A1.
 XX PD 06-MAR-2003.
 XX PF 28-AUG-2002; 2002US-00230338.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX DR WPI; 2003-492274/46.
 XX DR N-PSDB; ACD82195.
 XX PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 XX chromosome markers, or in generating probes.
 XX PS Claim 19; Fig 40; 315pp; English.
 XX CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. Nucleic acids that encode PRO can be used to generate either
 CC transgenic animals or knock-out animals useful in developing and
 CC screening of therapeutically useful reagents. The nucleic acids may also
 CC be used in gene therapy for replacing defective gene, in chromosome
 CC identification, as chromosome markers, or in generating probes to isolate
 CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
 CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
 CC and for detecting the presence of tumour in a mammal. The PRO
 CC polypeptides are useful as molecular markers for protein electrophoresis
 CC and the isolated nucleic acids may be used for recombinantly expressing
 CC those markers. The PRO polypeptides and nucleic acids may also be used in
 CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
 CC PRO and in affinity purification of PRO from recombinant cell culture or
 CC natural sources. The present sequence represents the amino acid sequence
 CC of a human secreted/transmembrane PRO polypeptide
 XX Sequence 290 AA;
 XX
 XX Query Match 99.6%; Score 1493; DB 6; Length 290;
 XX Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 XX Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLERSLTVCQVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLERSLTVCQVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQVYKDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNLDLGV 120
 Db 61 DCKILVKTSGSEQVYKDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNLDLGV 120
 QY 121 VQVITDPAVPTQETSSPTLTGHLNDRHKLKLSVLLPLITIXILLILVAASLLAWRM 180
 Db 121 VQVITDPAVPTQETSSPTLTGHLNDRHKLKLSVLLPLITIXILLILVAASLLAWRM 180
 QY 181 MKYQKAGMSPEQVLPFLEGDLCLADLTQLAGTSRKATTKLSSAQVDQVEVYVTA 240
 Db 181 MKYQKAGMSPEQVLPFLEGDLCLADLTQLAGTSRKATTKLSSAQVDQVEVYVTA 240
 QY 241 SLPKEDISYASLTIGADQETPCNWXLSXLPGRGPPEPTYSISR 290
 Db 241 SLPKEDISYASLTIGADQETPCNWXLSXLPGRGPPEPTYSISR 290

ABJ72077
 ID ABJ72077 standard; protein; 290 AA.
 XX AC ABJ72077;
 XX DT 16-OCT-2003 (first entry)
 XX DE Human membrane bound receptor/protein PRO10111 amino acid sequence.
 XX KW Human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX OS Homo sapiens.
 XX PI US2003065147-A1.
 XX PD 03-APR-2003.
 XX PF 29-AUG-2002; 2002US-00232224.
 XX PR 28-JUL-1999; 99US-0146222P.
 XX PR 24-FEB-2000; 2000WO-US005004.
 XX PR 02-MAR-2000; 2000WO-US005841.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX DR WPI; 2003-522018/49.
 XX DR N-PSDB; AB743901.
 XX PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for the manufacture of a medicament for diagnosing or treating
 XX tumor.
 XX PS Claim 11; Fig 40; 315pp; English.
 XX CC This invention relates to one hundred and twenty two novel nucleic acids
 CC encoding human PRO membrane bound proteins or receptors. Extracellular
 CC proteins play important roles in the formation, differentiation and
 CC maintenance of multicellular organisms. The fate of many individual cells
 CC (for example proliferation, migration or differentiation) is typically
 CC governed by information received from other cells and the immediate
 CC environment. The information is often transmitted by secreted
 CC polypeptides (for example mitogenic factors, survival factors, cytotoxic
 CC factors, differentiation factors, neurotrophic factors and hormones) which are
 CC received and interpreted by diverse cell receptors or membrane bound
 CC proteins. These membrane bound proteins and receptors may be of use as
 CC pharmaceutical and diagnostic agents, such as in the blocking of receptor
 CC -ligand interactions. The current invention provides the amino acid
 CC sequences of novel human membrane bound receptors and proteins, along
 CC with the cDNA sequences encoding them. The novel proteins of the
 CC invention may have cytostatic activities through the stimulation of
 CC chondrocytes. The nucleic acids of the invention may be useful for the
 CC manufacture of a medicament for diagnosing or treating a tumour in a
 CC mammal. In addition, they may be useful for measuring or detecting the
 CC expression of a tumour associated gene. The present sequence is the amino
 CC acid sequence of a human PRO protein of the invention
 XX Sequence 290 AA;
 XX
 XX Query Match 99.6%; Score 1493; DB 7; Length 290;
 XX Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 XX Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLSLTVQVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQVDRVSIHKNQKRTFTVMDLTKTDADTWGCIETGNDLGVY 120
 Db 61 DCKILVKTSGSEQVDRVSIHKNQKRTFTVMDLTKTDADTWGCIETGNDLGVY 120
 QY 121 VQVTTIDPAPVTOBETSSPFLTGHLNDRHKLKLSVLLPLIFITILLVVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOBETSSPFLTGHLNDRHKLKLSVLLPLIFITILLVVAASLLAWRM 180
 QY 181 MKYQQAAGSPQVLPQLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
 Db 181 MKYQQAAGSPQVLPQLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
 QY 241 SLPKEDISYASLTGAEDEQPTVCNMGHLSHLPGRGPEEPTETSTSRP 290
 Db 241 SLPKEDISYASLTGAEDEQPTVCNMGHLSHLPGRGPEEPTETSTSRP 290

RESULT 10

ADB83530

ID ADB83530 standard; protein; 290 AA.

XX AC ADB83530;

XX DT 04-DEC-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO10111.

XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;

XX KW antiarthritic; pericyte cell proliferation;

XX KW pericyte cell differentiation; chondrocyte cell proliferation;

XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;

XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;

XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;

XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;

XX KW gene therapy.

XX OS Homo sapiens.

XX FN US2003073814-A1.

XX FX 17-APR-2003.

XX FX 12-AUG-2002; 2002US-00218849.

XX FX 01-JUN-2001; 2001WO-US017800.

XX FX 29-JUN-2001; 2001WO-US021066.

XX FX 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Deenoyers L, Gerritsen MB, Goddard A, Godowski PU;

XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR WPI; 2003-644806/61.

XX DR N-PSDB; AD883529.

XX PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful

XX PT in gene therapy, chromosome identification, tissue typing, or as

XX PT hybridization probes in chromosome and gene mapping.

XX PS Claim 11; Fig 40; 315pp; English.

XX CC The invention describes an isolated PRO (secreted and transmembrane)

XX CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

XX CC useful for stimulating the proliferation of or gene expression in

XX CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

XX CC for stimulating the proliferation or differentiation of chondrocyte

XX CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide

XX CC are useful for stimulating the release of tumour necrosis factor (TNF)-

CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,

CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,

CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,

CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338,

CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1477, PRO1317, PRO1760, PRO1567,

CC PRO1887, PRO1928, PRO1341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4322,

CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for

CC stimulating the proliferation of normal human dermal fibroblasts cells.

CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,

CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC polypeptides such as PRO6004, PRO4981, PRO174, PRO5778, PRO4332, etc.,

CC are useful for detecting the presence of expression of the above PRO polypeptides

CC involves comparing the level of expression of the above PRO polypeptides

CC in a test sample of cells taken from the mammal, and a control sample of

CC normal cells of the same cell type, where a higher level of expression of

CC the PRO polypeptides in the test sample as compared to the control sample

CC is indicative of the presence of tumour in the mammal. The tumour is lung

CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or

CC liver tumour. (I) is useful as molecular weight markers, for tissue

CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is

CC useful for chromosome and gene mapping or gene therapy. (II) is useful

CC for generating transgenic animals or knock-out animals which are useful

CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide

CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,

CC sport injuries). This is the amino acid sequence of a human secreted and

CC transmembrane PRO polypeptide.

XX XX Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;

Best Local Similarity 99.0%; Pred. No. 9.8e-137;

Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLSLTVQVYRSGWETYLKWCRCGAIWR 60

Db 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLSLTVQVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEQVDRVSIHKNQKRTFTVMDLTKTDADTWGCIETGNDLGVY 120

Db 61 DCKILVKTSGSEQVDRVSIHKNQKRTFTVMDLTKTDADTWGCIETGNDLGVY 120

QY 121 VQVTTIDPAPVTOBETSSPFLTGHLNDRHKLKLSVLLPLIFITILLVVAASLLAWRM 180

Db 121 VQVTTIDPAPVTOBETSSPFLTGHLNDRHKLKLSVLLPLIFITILLVVAASLLAWRM 180

QY 181 MKYQQAAGSPQVLPQLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240

Db 181 MKYQQAAGSPQVLPQLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240

QY 241 SLPKEDISYASLTGAEDEQPTVCNMGHLSHLPGRGPEEPTETSTSRP 290

Db 241 SLPKEDISYASLTGAEDEQPTVCNMGHLSHLPGRGPEEPTETSTSRP 290

RESULT 11

ADB80636

ID ADB80636 standard; protein; 290 AA.

XX AC ADB80636;

XX DT 04-DEC-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO10111.

XX KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;

XX KW antiarthritic; pericyte cell proliferation;

XX KW pericyte cell differentiation; chondrocyte cell proliferation;

XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;

XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;

XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003088068-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 13-AUG-2002; 2002US-00219481.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2003-657982/62.
 DR N-PSDB; ADB73176.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 PS Claim 11; Fig 40; 305pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC are useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTLVLLFWLSGYSIATQITPTVNGLERSLTVQCYVRSGWETYLKWCRCGAIWR 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MPLLTLLVLLFWLSGYSIATQITPTVNGLERSLTVQCYVRSGWETYLKWCRCGAIWR 60
 QY 61 DKILVKTSGEQVXRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DKILVKTSGEQVXRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 QY 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLFTITKLLLVAAASLAWRM 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLFTITKLLLVAAASLAWRM 180
 QY 181 MKYQQAAGMSPEVLOPLEGLDLYADLTQLAGTSPKATKLSAODVQVEVEYTTWA 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 MKYQQAAGMSPEVLOPLEGLDLYADLTQLAGTSPKATKLSAODVQVEVEYTTWA 240
 QY 241 SLPKEDISYASLTGAEDQEPYCNMGLSSXLPGRGPPEPTEYSTISRP 290
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 SLPKEDISYASLTGAEDQEPYCNMGLSSXLPGRGPPEPTEYSTISRP 290
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 12
 ADB73177
 ID ADB73177 standard; protein; 290 AA.
 XX
 AC ADB73177;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10111.
 XX
 KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 US2003096968-A1.
 XX
 PN 22-MAY-2003.
 XX
 PD 29-AUG-2002; 2002US-00232223.
 PF
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2003-765525/72.
 DR N-PSDB; ADB73176.
 XX
 PT New isolated PRO polypeptides useful as molecular weight markers in
 PT protein electrophoresis, useful for tissue typing, and for treating
 PT arthritis and tumors.
 XX
 PS Claim 11; Fig 40; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC are useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX

CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408.
 CC PRO5723, PRO5725, PRO1154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERSLTVCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERSLTVCVYRSGWETYLKWCRCGAIWR 60
 Qy 61 DCKILVTSSEQVEKDRVSKDKNKNRTFTVMEIDMKTDADTYWCGLEKTNGLVGT 120
 Db 61 DCKILVTSSEQVEKDRVSKDKNKNRTFTVMEIDMKTDADTYWCGLEKTNGLVGT 120
 Qy 121 VQVITDPAPVQETSSPTTGHLDNRHKLKSLVLLPLFIIXLLLVAAASLLAWRM 180
 Db 121 VQVITDPAPVQETSSPTTGHLDNRHKLKSLVLLPLFIIXLLLVAAASLLAWRM 180
 Qy 181 MKYQKAGMSPQVLOPLEGDLCYADLTQLAGTSRKAATKLSQAQVQVEVEYVTMA 240
 Db 181 MKYQKAGMSPQVLOPLEGDLCYADLTQLAGTSRKAATKLSQAQVQVEVEYVTMA 240
 Qy 241 SLPKEDISYASLTGAEDEPTYNMGHLSXLPGRGPEEPTYSTISRP 290
 Db 241 SLPKEDISYASLTGAEDEPTYNMGHLSXLPGRGPEEPTYSTISRP 290
 RESULT 13
 ADB78259
 ID ADB78259 standard; protein; 290 AA.
 XX
 AC ADB78259;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
 KW antiarthritis; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;

KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003092889-A1.
 XX 15-MAY-2003.
 PD
 XX 13-AUG-2002; 2002US-00219478.
 PF
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021056.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-765495/72.
 DR N-PSDB; ADB78258.
 DR
 XX New isolated PRO polypeptide useful for tissue typing, gene therapy, as
 PT molecular weight markers in protein electrophoresis, and for treating
 PT arthritis and tumors.
 XX
 PS Claim 11; Fig 40; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERSLTVCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLTYLLFLWLSGYSIATQITGPTTVNGLERSLTVCVYRSGWETYLKWCRCGAIWR 60

CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.

XX
SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERSLTQCVYRSGWETYLKWCAGAIWR 60
DB 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERSLTQCVYRSGWETYLKWCAGAIWR 60
QY 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPIFTIXLLLVAAASLLAWRM 180
DB 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGSPROVLQPLEGDLQYADLTLOLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQQAAGSPROVLQPLEGDLQYADLTLOLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYCNMGXLSXLPGRGPEEPTXTISRP 290
DB 241 SLPKEDISYASLTGAEDEPTCYCNMGXLSXLPGRGPEEPTXTISRP 290

RESULT 15
ADB84907
ID ADB84907 standard; protein; 290 AA.
XX
AC ADB84907;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #20.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
KW cancer; lung; colon; breast; prostate; rectum; liver;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW arthritis; sports injury; cytostatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003073817-A1.
XX
PD 17-APR-2003.
XX
PF 26-AUG-2002; 2002US-00227883.
XX
PR 01-AUG-2000; 2000US-0222425P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI, 2003-730024/69.
DR N-PSDB; ADB84906.
XX
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT e.g. in gene therapy, disease diagnosis, chromosome identification and
PT tissue typing.
XX
PS Claim 11; Fig 40; 314pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. They are particularly useful for
CC detecting tumours (e.g. lung tumour; colon tumour; breast tumour,
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
CC blood, for stimulating the proliferation or differentiation of
CC chondrocyte cells, for stimulating the proliferation of or gene
CC expression in pericyte cells or for stimulating the proliferation of
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
CC hybridisation probes, in chromosome and gene mapping, in generating

CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.

XX
SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERSLTQCVYRSGWETYLKWCAGAIWR 60
DB 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERSLTQCVYRSGWETYLKWCAGAIWR 60
QY 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPIFTIXLLLVAAASLLAWRM 180
DB 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGSPROVLQPLEGDLQYADLTLOLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQQAAGSPROVLQPLEGDLQYADLTLOLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYCNMGXLSXLPGRGPEEPTXTISRP 290
DB 241 SLPKEDISYASLTGAEDEPTCYCNMGXLSXLPGRGPEEPTXTISRP 290

RESULT 15
ADB78013
ID ADB78013 standard; protein; 290 AA.
XX
AC ADB78013;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10111.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003092886-A1.
XX
PD 15-MAY-2003.
XX
PF 09-AUG-2002; 2002US-00216165.
XX
PR 25-JUL-2000; 2000US-0220607P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX

(GETH) GENENTECH INC. Db 241 SLPKEDISYASLTILGAEDQETPCYCNMGXLSXSLFGRGPEETPEYTSISR 290

PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
FI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI, 2003-765494/72.
DR N-PSDB; ADB78012.
XX

XX Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as
PT molecular weight markers in protein electrophoresis, for treating
PT arthritis, tumor.

XX Claim 11; Fig 40; 308pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1274, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.

XX Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;
Best Local Similarity 99.0%; Pred.No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPLILTLVLLFWLSGYSIATQITPTTVNGLERGLTVQCVYRSGWETYLKMWCRGAIWR 60
Db 1 MPELLTLVLLFWLSGYSIATQITPTTVNGLERGLTVQCVYRSGWETYLKMWCRGAIWR 60
Qy 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTWMDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTWMDLMKTDADTYWCGIEKTGNDLGVT 120
Qy 121 VQVITDPAVPTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIKLLLVAASSLAWRM 180
Db 121 VQVITDPAVPTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIKLLLVAASSLAWRM 180
Qy 181 MKYQKAGMSPQVQLPLEGDLVADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKAGMSPQVQLPLEGDLVADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
Qy 241 SLPKEDISYASLTILGAEDQETPCYCNMGXLSXSLFGRGPEETPEYTSISR 290

Search completed: September 16, 2004, 12:37:17
Job time : 125 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:39:56 ; Search time 131 Seconds
(without alignments)
710.906 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
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Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 32113274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1493	99.6	290	9	US-09-965-529-18
2	1493	99.6	290	10	US-09-969-680A-18
3	1493	99.6	290	12	US-10-219-535-40
4	1493	99.6	290	12	US-10-232-230-40
5	1493	99.6	290	12	US-10-232-224-40
6	1493	99.6	290	14	US-10-227-884-40
7	1493	99.6	290	14	US-10-230-163-40
8	1493	99.6	290	14	US-10-230-338-40
9	1493	99.6	290	14	US-10-218-631-40
10	1493	99.6	290	14	US-10-230-414-40
11	1493	99.6	290	14	US-10-216-159A-40
12	1493	99.6	290	14	US-10-218-849-40
13	1493	99.6	290	14	US-10-227-873-40
14	1493	99.6	290	14	US-10-227-883-40
15	1493	99.6	290	14	US-10-219-076-40

16	1493	99.6	290	14	US-10-230-434-40
17	1493	99.6	290	14	US-10-219-003-40
18	1493	99.6	290	14	US-10-219-075-40
19	1493	99.6	290	14	US-10-213-484-40
20	1493	99.6	290	14	US-10-219-466-40
21	1493	99.6	290	14	US-10-219-479-40
22	1493	99.6	290	14	US-10-219-481-40
23	1493	99.6	290	14	US-10-230-260-40
24	1493	99.6	290	14	US-10-232-231-40
25	1493	99.6	290	14	US-10-232-233-40
26	1493	99.6	290	14	US-10-216-185-40
27	1493	99.6	290	14	US-10-218-956-40
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29	1493	99.6	290	14	US-10-219-478-40
30	1493	99.6	290	14	US-10-219-536-40
31	1493	99.6	290	14	US-10-233-205-40
32	1493	99.6	290	14	US-10-219-072-40
33	1493	99.6	290	14	US-10-213-470-40
34	1493	99.6	290	14	US-10-219-474-40
35	1493	99.6	290	14	US-10-219-524-40
36	1493	99.6	290	14	US-10-219-528-40
37	1493	99.6	290	14	US-10-227-880-40
38	1493	99.6	290	14	US-10-227-881-40
39	1493	99.6	290	14	US-10-227-882-40
40	1493	99.6	290	14	US-10-230-436-40
41	1493	99.6	290	14	US-10-232-223-40
42	1493	99.6	290	14	US-10-232-225-40
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ALIGNMENTS

RESULT 1
US-09-965-529-18
; Sequence 18, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyrng Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1562471CD1
US-09-965-529-18

Query Match 99.6%; Score 1493; DB 9; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPLLTYLLFWLSGYSIATQITGPTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTYLLFWLSGYSIATQITGPTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVMA 240
 Db 181 MKYQQAAGMSPEQVLPQLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVMA 240
 QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290
 Db 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290

RESULT 2

US-09-969-680A-18
 ; Sequence 18, Application US/09969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969,680A
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US00/22315
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149,641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164,203
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 18
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 1562471CD1
 US-09-969-680A-18

Query Match 99.6%; Score 1493; DB 10; Length 290;
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 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVMA 240
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 Db 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290

RESULT 3
 US-10-219-535-40
 ; Sequence 40, Application US/10219535
 ; Publication No. US20040044179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3530PIC60
 ; CURRENT APPLICATION NUMBER: US/10/219,535
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 40
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-219-535-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
 Best Local Similarity 99.0%; Pred. No. 2.9e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTYLLLFWSLGSYIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTYLLLFWSLGSYIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVMA 240
 Db 181 MKYQQAAGMSPEQVLPQLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVMA 240
 QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290
 Db 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290

Db 241 SLPKEDISYASLTGAEDEPTCYCNMGHLSHLPGRGPEEPTYSTISRP 290

RESULT 4

US-10-232-230-40
; Sequence 40, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C103
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVQTESSPTTGHLDNRHKLKLSVLLPLFTIXLLLVAAALLAWRM 180
Db 121 VQVTTIDPAPVQTESSPTTGHLDNRHKLKLSVLLPLFTIXLLLVAAALLAWRM 180
QY 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYCNMGHLSHLPGRGPEEPTYSTISRP 290

RESULT 5

US-10-232-224-40
; Sequence 40, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVQTESSPTTGHLDNRHKLKLSVLLPLFTIXLLLVAAALLAWRM 180
Db 121 VQVTTIDPAPVQTESSPTTGHLDNRHKLKLSVLLPLFTIXLLLVAAALLAWRM 180
QY 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYCNMGHLSHLPGRGPEEPTYSTISRP 290

Db 241 SLPKEDISASLTGAEDEPTVCNMGHLSHLPGRGPEETEXTSTSRP 290
RESULT 6
US-10-227-884-40
; Sequence 40, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

QY 121 VQVTTIDPAPVTOEBTSSPTLTGHLDNRHKLKLVLLPFIITXILLVVAASLLAWRM 180
DB 121 VQVTTIDPAPVTOEBTSSPTLTGHLDNRHKLKLVLLPFIITXILLVVAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLQPLEGLDLCYADLTQLAGTSRKATTKLSSAQDVQVEYVYVMA 240
DB 181 MKYQOKAAGMSPEQVLQPLEGLDLCYADLTQLAGTSRKATTKLSSAQDVQVEYVYVMA 240
QY 241 SLPKEDISYASLTGAEDEPTYCNMGXLSXLPFGRGPEEPTETYSISR 290
DB 241 SLPKEDISYASLTGAEDEPTYCNMGHLSHLFGRGPEEPTETYSISR 290

RESULT 7
US-10-230-163-40
; Sequence 40, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PLC96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905

PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTYLLFLWLSGYSATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTYLLFLWLSGYSATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/098596
PRIOR FILING DATE: 1998-09-03
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
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PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIAQTITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTYLLFWLSGYSIAQTITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
QY 121 VQVITDPAPVQTBETSSPTLTGHHLNDRHKLKLSVLLPLFIETIXLLLLVAASLLAWRM 180
Db 121 VQVITDPAPVQTBETSSPTLTGHHLNDRHKLKLSVLLPLFIETIXLLLLVAASLLAWRM 180
QY 181 MKYQKRAAGMSPQVLOPLEGDIQYADLTLOLAGTSRKAATTKLSSAQVDQVEVEYV 240
Db 181 MKYQKRAAGMSPQVLOPLEGDIQYADLTLOLAGTSRKAATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTGAEQDEPTCYNMGKLSXLPGRGPPEEPTYSISR 290
Db 241 SLPKEDISYASLTGAEQDEPTCYNMGKLSXLPGRGPPEEPTYSISR 290

RESULT 8
US-10-230-338-40
; Sequence 40, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/052287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-40

Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTYLLFWLSGYSIAQTITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTYLLFWLSGYSIAQTITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
QY 121 VQVITDPAPVQTBETSSPTLTGHHLNDRHKLKLSVLLPLFIETIXLLLLVAASLLAWRM 180
Db 121 VQVITDPAPVQTBETSSPTLTGHHLNDRHKLKLSVLLPLFIETIXLLLLVAASLLAWRM 180
QY 181 MKYQKRAAGMSPQVLOPLEGDIQYADLTLOLAGTSRKAATTKLSSAQVDQVEVEYV 240
Db 181 MKYQKRAAGMSPQVLOPLEGDIQYADLTLOLAGTSRKAATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTGAEQDEPTCYNMGKLSXLPGRGPPEEPTYSISR 290
Db 241 SLPKEDISYASLTGAEQDEPTCYNMGKLSXLPGRGPPEEPTYSISR 290

RESULT 9
US-10-218-631-40
; Sequence 40, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-40

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;

Query Match 99.6%; Score 1493; DB 14; Length 290;

	Best Local Similarity	99.0%;	Pred. No. 2.9e-137;	Mismatches	0;	Gaps	0;
	Matches	287;	Conservative	0;	Indels	0;	
Qy	1	MPLLTLYLLFWLSGYSIAT	IGPTTNGLERGSLTVQCVYRSGWNTY	LKWCRCGAIWR	60		
Db	1	MPLLTLYLLFWLSGYSIAT	IGPTTNGLERGSLTVQCVYRSGWNTY	LKWCRCGAIWR	60		
Qy	61	DKCILVKTSGSEQEVRKDRVSI	KDNQKRTFTVTMEDLMKTDADTY	WCGIEKTDNLGVT	120		
Db	61	DKCILVKTSGSEQEVRKDRVSI	KDNQKRTFTVTMEDLMKTDADTY	WCGIEKTDNLGVT	120		
Qy	121	VQVITIDPAPVTOETSSPTLT	GHHLDNRHKLKLSVLLPLIFITIKLLLVAA	SLLAWRM	180		
Db	121	VQVITIDPAPVTOETSSPTLT	GHHLDNRHKLKLSVLLPLIFITIKLLLVAA	SLLAWRM	180		
Qy	181	MKYQOKAAGMSPEOVLP	LEGDLCYADTLQLAGTS	SPRKATTKLSSAQVDQVEYVTMA	240		
Db	181	MKYQOKAAGMSPEOVLP	LEGDLCYADTLQLAGTS	SPRKATTKLSSAQVDQVEYVTMA	240		
Qy	241	SLPKEDISYASLTUGADQDEPT	YCNMGKLSKXLPGRGPEETPEY	TSYTSRSP	290		
Db	241	SLPKEDISYASLTUGADQDEPT	YCNMGHLSHLPRGPERPEY	TSYTSRSP	290		

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RESULT 11
; US-10-216-159A-40
; Sequence 40, Application US/10216:159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-216-159A-40

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Query Match      99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MPELTLYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db      1  MPELTLYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY      61  DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGVT 120
Db      61  DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGVT 120

QY      121  VQVITDPAPVQEBTSSPTTGHLDNRHKLKLSVLLPLIFTIIXLLLVAAASLLAWRM 180
Db      121  VQVITDPAPVQEBTSSPTTGHLDNRHKLKLSVLLPLIFTIIXLLLVAAASLLAWRM 180

QY      181  MKYQQAAGMSPEQVLQPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
Db      181  MKYQQAAGMSPEQVLQPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240

QY      241  SLPKEDISYASLTIGAEDQPTVCNMGXLSXLPGRGPPEPTYSTISRP 290
Db      241  SLPKEDISYASLTIGAEDQPTVCNMGXLSXLPGRGPPEPTYSTISRP 290

RESULT 12
US-10-218-849-40
; Sequence 40, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218.849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-40

Query Match      99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  MPELTLYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db      1  MPELTLYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY      61  DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGVT 120
Db      61  DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGVT 120

QY      121  VQVITDPAPVQEBTSSPTTGHLDNRHKLKLSVLLPLIFTIIXLLLVAAASLLAWRM 180
Db      121  VQVITDPAPVQEBTSSPTTGHLDNRHKLKLSVLLPLIFTIIXLLLVAAASLLAWRM 180

QY      181  MKYQQAAGMSPEQVLQPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
Db      181  MKYQQAAGMSPEQVLQPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
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Db      181  MKYQQAAGMSPEQVLQPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTMA 240
QY      241  SLPKEDISYASLTIGAEDQPTVCNMGXLSXLPGRGPPEPTYSTISRP 290
Db      241  SLPKEDISYASLTIGAEDQPTVCNMGXLSXLPGRGPPEPTYSTISRP 290

RESULT 13
US-10-227-873-40
; Sequence 40, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227.873
; CURRENT FILING DATE: 2002-08-26
; Prior Application Number: 10/119,480
; Prior Filing Date: 2002-04-09
; Prior Application Number: 60/059113
; Prior Filing Date: 1997-09-17
; Prior Application Number: 60/062287
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063549
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/069873
; Prior Filing Date: 1997-12-17
; Prior Application Number: 60/078910
; Prior Filing Date: 1998-03-20
; Prior Application Number: 60/079294
; Prior Filing Date: 1998-03-25
; Prior Application Number: 60/079656
; Prior Filing Date: 1998-03-26
; Prior Application Number: 60/079728
; Prior Filing Date: 1998-03-27
; Prior Application Number: 60/081819
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/081955
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/082804
; Prior Filing Date: 1998-04-22
; Prior Application Number: 60/084441
; Prior Filing Date: 1998-05-06
; Prior Application Number: 60/085323
; Prior Filing Date: 1998-05-13
; Prior Application Number: 60/085579
; Prior Filing Date: 1998-05-15
; Prior Application Number: 60/086392
; Prior Filing Date: 1998-05-22
; Prior Application Number: 60/089532
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089538
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089905
; Prior Filing Date: 1998-06-18
; Prior Application Number: 60/090472
; Prior Filing Date: 1998-06-24
; Prior Application Number: 60/090557
; Prior Filing Date: 1998-06-24
; Prior Application Number: 60/090691
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;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090695
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/091982
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/095302
;	PRIOR FILING DATE:	1998-08-04
;	PRIOR APPLICATION NUMBER:	60/095318
;	PRIOR FILING DATE:	1998-08-04
;	PRIOR APPLICATION NUMBER:	60/095916
;	PRIOR FILING DATE:	1998-08-10
;	PRIOR APPLICATION NUMBER:	60/096146
;	PRIOR FILING DATE:	1998-08-11
;	PRIOR APPLICATION NUMBER:	60/096791
;	PRIOR FILING DATE:	1998-08-17
;	PRIOR APPLICATION NUMBER:	60/097986
;	PRIOR FILING DATE:	1998-08-26
;	PRIOR APPLICATION NUMBER:	60/098544
;	PRIOR FILING DATE:	1998-08-31
;	PRIOR APPLICATION NUMBER:	60/099596
;	PRIOR FILING DATE:	1998-09-09
;	PRIOR APPLICATION NUMBER:	60/099598
;	PRIOR FILING DATE:	1998-09-09
;	PRIOR APPLICATION NUMBER:	60/099803
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099811
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099812
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/099916
;	PRIOR FILING DATE:	1998-09-10
;	PRIOR APPLICATION NUMBER:	60/100038
;	PRIOR FILING DATE:	1998-09-11
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;	PRIOR FILING DATE:	1998-09-15
;	PRIOR APPLICATION NUMBER:	60/100390
;	PRIOR FILING DATE:	1998-09-15
;	PRIOR APPLICATION NUMBER:	60/100627
;	PRIOR FILING DATE:	1998-09-16
;	PRIOR APPLICATION NUMBER:	60/100848
;	PRIOR FILING DATE:	1998-09-18
;	PRIOR APPLICATION NUMBER:	60/100919
;	PRIOR FILING DATE:	1998-09-17
;	PRIOR APPLICATION NUMBER:	60/101477
;	PRIOR FILING DATE:	1998-09-23
;	PRIOR APPLICATION NUMBER:	60/101738
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101741
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101786
;	PRIOR FILING DATE:	1998-09-25
;	PRIOR APPLICATION NUMBER:	60/101916
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101922
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/106178
;	PRIOR FILING DATE:	1998-10-28
;	PRIOR APPLICATION NUMBER:	60/106248
;	PRIOR FILING DATE:	1998-10-29
;	PRIOR APPLICATION NUMBER:	60/106464
;	PRIOR FILING DATE:	1998-10-30
;	PRIOR APPLICATION NUMBER:	60/106905
;	PRIOR FILING DATE:	1998-11-03
;	PRIOR APPLICATION NUMBER:	60/108787
;	PRIOR FILING DATE:	1998-11-17
;	PRIOR APPLICATION NUMBER:	60/108801
;	PRIOR FILING DATE:	1998-11-17
;	PRIOR APPLICATION NUMBER:	60/108849
;	PRIOR FILING DATE:	1998-11-18
;	PRIOR APPLICATION NUMBER:	60/112422
;	PRIOR FILING DATE:	1998-12-15
;	PRIOR APPLICATION NUMBER:	60/113296
;	PRIOR FILING DATE:	1998-12-22

7	PRIOR APPLICATION NUMBER: 60/1136050
7	PRIOR FILING DATE: 1998-12-23
7	PRIOR APPLICATION NUMBER: 60/113621
7	PRIOR FILING DATE: 1998-12-23
7	PRIOR APPLICATION NUMBER: 60/115558
7	PRIOR FILING DATE: 1999-01-12
7	PRIOR APPLICATION NUMBER: 60/115565
7	PRIOR FILING DATE: 1999-01-12
7	PRIOR APPLICATION NUMBER: 60/115733
7	PRIOR FILING DATE: 1999-01-12
7	PRIOR APPLICATION NUMBER: 60/119549
7	PRIOR FILING DATE: 1999-02-10
7	PRIOR APPLICATION NUMBER: 60/123618
7	PRIOR FILING DATE: 1999-03-10
7	PRIOR APPLICATION NUMBER: 60/125259
7	PRIOR FILING DATE: 1999-03-19
7	PRIOR APPLICATION NUMBER: 60/125775
7	PRIOR FILING DATE: 1999-03-23
7	PRIOR APPLICATION NUMBER: 60/126773
7	PRIOR FILING DATE: 1999-03-29
7	PRIOR APPLICATION NUMBER: 60/127887
7	PRIOR FILING DATE: 1999-04-05
7	PRIOR APPLICATION NUMBER: 60/130232
7	PRIOR FILING DATE: 1999-04-21
7	PRIOR APPLICATION NUMBER: 60/131022
7	PRIOR FILING DATE: 1999-04-26
7	PRIOR APPLICATION NUMBER: 60/131270
7	PRIOR FILING DATE: 1999-04-27
7	PRIOR APPLICATION NUMBER: 60/131291
7	PRIOR FILING DATE: 1999-04-27
7	PRIOR APPLICATION NUMBER: 60/131445
7	PRIOR FILING DATE: 1999-04-28
7	PRIOR APPLICATION NUMBER: 60/134287
7	PRIOR FILING DATE: 1999-05-14
7	PRIOR APPLICATION NUMBER: 60/140650
7	PRIOR FILING DATE: 1999-06-22
7	PRIOR APPLICATION NUMBER: 60/140723
7	PRIOR FILING DATE: 1999-06-22
7	PRIOR APPLICATION NUMBER: 60/141037
7	PRIOR FILING DATE: 1999-06-23
7	PRIOR APPLICATION NUMBER: 60/144758
7	PRIOR FILING DATE: 1999-07-20
7	PRIOR APPLICATION NUMBER: 60/145698
7	PRIOR FILING DATE: 1999-07-26
7	PRIOR APPLICATION NUMBER: 60/146222
7	PRIOR FILING DATE: 1999-07-28
7	PRIOR APPLICATION NUMBER: 60/146963
7	PRIOR FILING DATE: 1999-08-03
7	PRIOR APPLICATION NUMBER: 60/149320
7	PRIOR FILING DATE: 1999-08-17
7	PRIOR APPLICATION NUMBER: 60/149638
7	PRIOR FILING DATE: 1999-08-17
7	PRIOR APPLICATION NUMBER: 60/151733
7	PRIOR FILING DATE: 1999-08-31
7	PRIOR APPLICATION NUMBER: 60/164418
7	PRIOR FILING DATE: 1999-11-09
7	PRIOR APPLICATION NUMBER: 60/166361
7	PRIOR FILING DATE: 1999-11-16
7	PRIOR APPLICATION NUMBER: 60/169445
7	PRIOR FILING DATE: 1999-12-07
7	PRIOR APPLICATION NUMBER: 60/169495
7	PRIOR FILING DATE: 1999-12-07
7	PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0

[illegible]

Db 61 DCKILVKTSGSQEVKRDVSKDKQKRTFTVTWEDLMKTDADTYWCGIETGNDLGV 120
QY 121 VQVTTDPAPVTOBETSSSTLTGHLDNRHKLKLSVLLPLFTITXLLVAASLLAWRM 180
Db 121 VQVTTDPAPVTOBETSSSTLTGHLDNRHKLKLSVLLPLFTITXLLVAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLOPLEGDLVADITLQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLOPLEGDLVADITLQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISVASLTGAEDQEPYCNMGXLSXLPGRGPPEPTXSTISRP 290
Db 241 SLPKEDISVASLTGAEDQEPYCNMGXLSXLPGRGPPEPTXSTISRP 290

RESULT 14

US-10-227-883-40
; Sequence 40, Application US/10227883
; Publication No. US2003007387A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530F1C78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-04-15
; PRIOR FILING DATE: 1998-04-15
; PRIOR FILING DATE: 1998-04-22
; PRIOR FILING DATE: 1998-05-06
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 1998-05-15
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
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; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
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; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
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; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787

;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
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;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149638
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db |||||||
QY 61 DCKILVKTSGSQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db |||||||
QY 61 DCKILVKTSGSQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db |||||||
QY 121 VQVTTDPAPVTOBETSSPTLGHLDNRHKLKLVLLPLFTTILLLVAASLLAWRM 180
Db |||||||
QY 181 MKYQKKAAGMSPEQVLQPLEGDLQVADLTQLAGTSPRKATTKLSSAQVDQVEVEYV 240
Db |||||||
QY 241 SLPKEDISYASLTGAEDOEPTYCNMGLSSHLPGRGPEEPTSTISRP 290
Db |||||||

RESULT 15
US-10-219-076-40
;; Sequence 40, Application US/10219076
;; Publication No. US20030078379A1
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Philippe F.
;; APPLICANT: Watanabe, Colin L.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3530FIC62
;; CURRENT APPLICATION NUMBER: US/10/219,076
;; PRIOR FILING DATE: 2002-08-14
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO 40
;; LENGTH: 290
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-219-076-40


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Query Match      99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLYLLFLWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLYLLFLWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120

QY 121 VQVTIDPAPVTQBEETSSPTLTGHLDNRHKLKLSVLLPLIPTIXKLLLVAAASLIAMRM 180
Db 121 VQVTIDPAPVTQBEETSSPTLTGHLDNRHKLKLSVLLPLIPTIXKLLLVAAASLIAMRM 180

QY 181 MKYQOKAAGNSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQOKAAGNSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISVASLTIGAEDQEPPTYCMMGXLSXLPGRGPPEPTTEYSTISR 290
Db 241 SLPKEDISVASLTIGAEDQEPPTYCMMGXLSXLPGRGPPEPTTEYSTISR 290
```

Search completed: September 16, 2004, 12:51:46
Job time : 133 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2004, 12:32:35 ; Search time 41 Seconds
(without alignments)
680.379 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPLLTYLLFLWLSGVSIAT.....SXLPGRGPEPTYSTISRP 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	231	15.4	228	JC7761	dendritic cell-der
2	224.5	15.0	224	I37243	CMRF-35 antigen -
3	159.5	10.6	773	QRREG	secretory componen
4	145.5	9.7	769	QRRTGS	secretory componen
5	134.5	9.0	764	QRHUGS	secretory componen
6	132.5	8.8	757	S48841	polymERIC immunogl
7	131.5	8.8	757	I45956	T-cell receptor de
8	129.5	8.6	292	S03421	T-cell receptor de
9	128.5	8.5	142	S04654	T-cell receptor de
10	127.5	8.5	293	A40311	T-cell receptor de
11	127	8.5	157	S04915	rearranged T-cell
12	126.5	8.4	138	I46634	rearranged T-cell
13	126	8.4	137	I46628	rearranged T-cell
14	125	8.3	145	I46633	rearranged T-cell
15	124.5	8.3	131	S36301	T-cell receptor de
16	119.5	8.0	115	B32071	T-cell receptor de
17	116.5	7.8	135	S36288	T-cell receptor de
18	115.5	7.7	142	S36316	T-cell receptor de
19	115.5	7.7	145	S36239	T-cell receptor de
20	115.5	7.7	149	S36317	T-cell receptor de
21	114.5	7.6	146	S36323	T-cell receptor de
22	110.5	7.4	143	S36300	T-cell receptor de
23	108.5	7.2	132	I46640	rearranged T-cell
24	108.5	7.2	136	I46635	T-cell receptor de
25	108.5	7.2	137	S36311	T-cell receptor de
26	107.5	7.2	143	S36321	T-cell receptor de
27	106.5	7.1	142	S36310	T-cell receptor de
28	106.5	7.1	142	S36309	T-cell receptor de
29	105	7.0	151	I46626	rearranged T-cell

30	105	7.0	271	2	A53268	T-cell receptor al
31	105	7.0	451	2	S71754	cellular hepatitis
32	104.5	7.0	142	2	S36307	T-cell receptor de
33	104.5	7.0	145	2	I46629	rearranged T-cell
34	104.5	7.0	145	2	I46639	rearranged T-cell
35	102	6.8	128	2	S46372	IG light chain var
36	101	6.7	139	2	I46630	rearranged T-cell
37	99.5	6.6	133	2	I46632	rearranged T-cell
38	99	6.6	129	1	KIHUWK	IG kappa chain pre
39	99	6.6	143	2	JI0082	T-cell receptor de
40	99	6.6	841	2	JC5894	killer cell inhibi
41	98.5	6.6	120	2	S36306	T-cell receptor de
42	98.5	6.6	135	2	S57892	T-cell receptor de
43	98.5	6.6	144	2	S36308	T-cell receptor de
44	98.5	6.6	145	2	I46631	rearranged T-cell
45	98.5	6.6	1694	2	S50065	sialoadhesin - mou

ALIGNMENTS

RESULT 1

JC7761
dendritic cell-derived immunoglobulin(Ig)-like receptor 1.DIGR1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7761
R:luo, K.; Zhang, W.; Sui, L.; Li, N.; Zhang, M.; Ma, X.; Zhang, L.; Cao, X.
Biochem. Biophys. Res. Commun. 287, 35-41, 2001
A:Title: DIGR1, a novel membrane receptor of the immunoglobulin gene superfamily, is pre
A:Reference number: JC7761; PMID:11549249
A:Contents: Dendritic cells
A:Accession: JC7761
A:Molecule type: mRNA
A:Residues: 1-228 <LUO>
A:Cross-references: GB:AY048685
C:Comment: This protein, a cell surface type I transmembrane glycoprotein of membrane re
functions in the immunobiology of antigen-presenting cells.
C:Genetics:
A:Gene: digr1
C:Keywords: glycoprotein

Query Match	15.4%	Score	231;	DB	2;	Length	228;
Best Local Similarity	36.7%	Pred.	No. 6.6e-12;				
Matches	58;	Conservative	26;	Mismatches	52;	Indels	22;
Gaps	6;						
QY	8	LLLFMLSGVSIATQLT	-----GPTVANGLRGSLTVOCVYRSGWETVLKWCGRGAIWRD	61			
Db	5	VIRLWLPNALFLSQVPGCVPLHGPSTITGAVCESLSVSCQYEKFKTKDKFCWCRSLKVL	64				
QY	62	CKILVKTSGEQVXRDRVSKDNOKNETFTVTMBDLMKTDADTYWCGB	-----KTGN	115			
Db	65	CKDIVKTSSE-EVANGRVTRDHPDNLFTVTYBSLTLEDADTYMCAVDISLGDGSLGF	123				
QY	116	DLGVTVOVTIDFA--PVTQETSS-----SPTLT-GH	144				
Db	124	DKYFKIELSVSPEDPVTGSSLESGRDILESPTSSVGH	161				

RESULT 2

I37243
CMRF-35 antigen - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I37243
R:Jackson, D.G.; Hart, D.N.; Starling, G.; Bell, J.I.
Eur. J. Immunol. 22, 1157-1163, 1992
A:Title: Molecular cloning of a novel member of the immunoglobulin gene superfamily homo
A:Reference number: I37243; PMID:1349532
A:Accession: I37243
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-224 <RES>

Db 180 TEYVDPYKORAILFMKGTSDIFVYNISHLISDAGLYVCO-----AGSGPSADKN 231

Qy 194 ----QVLOP-EGDL-CYADLTQQA-----GTSRKATKLSQAQVQVVEYVTMAS--- 241

Db 232 NADLOVLEP-EPELLYKDLRSSVTFECDLGREVANDAKYLCRNKKTCDVIINTLGRDP 290

Qy 242 -----LPKEDIS-YASLTLAGDEDEPYCNKXGLSSXLPGRG 277

Db 291 AFEGRILLTPDDNGRFSVLITGRKEDAGHYQCGAUSSLGLPQEG 335

RESULT 5

ORHUGS

A:Title: secretory component precursor [validated] - human

N:Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

K:Contains: free secretory component; transmembrane secretory component

C:Species: Homo sapiens (man)

C/Date: 28-Aug-1985 #sequence revision 23-Aug-1996 #text_change 08-Dec-2000

C/Accession: A46537; A55284; I38115; A32263; S38978; S13453; A02112

R:Krajci, P.; Kvale, D.; Tasken, K.; Brandtzaeg, P.

Eur. J. Immunol. 22, 2309-2315, 1992

A:Title: Molecular cloning and exon-intron mapping of the gene encoding human transmembrane secretory component

A/Reference number: A46537; MUID:92387236; PMID:1335431

A/Accession: A46537

A/Status: not compared with conceptual translation

A:Molecule type: DNA

A/Residues: 1-764 <KRA>

A/Cross-references: GB:5434449; NID:G255097; PIDN:AB23176.1; PID:G255098

A/Experimental source: leukocytes

A/Note: sequence extracted from NCBI backbone (NCBIP:113253)

R:Krajci, P.; Grzeschik, K.H.; Geurts van Kessel, A.H.; Olaisen, B.; Brandtzaeg, P.

Hum. Genet. 87, 642-648, 1991

A:Title: The human transmembrane secretory component (poly-Ig receptor): molecular cloning

A/Reference number: A55284; MUID:92039621; PMID:1682231

A/Accession: A55284

A:Molecule type: mRNA

A/Residues: 1-764 <KR2>

A/Cross-references: GB:562403; NID:G238235; PIDN:AA20203.1; PID:G238236

A/Experimental source: colonic adenocarcinoma cell line

A/Note: sequence extracted from NCBI backbone (NCBIN:62408)

R:Piskurich, J.F.; France, J.A.; Tamer, C.M.; Willmer, C.A.; Kaetzal, D.M.

Mol. Immunol. 30, 413-421, 1993

A:Title: Interferon-gamma induces polymeric immunoglobulin receptor mRNA in human intest

A/Reference number: I38115; MUID:93205018; PMID:8455639

A/Accession: I38115

A:Molecule type: mRNA

A/Residues: 1-764 <RES>

A/Cross-references: EMBL:X73079; NID:G456345; PIDN:CAA51532.1; PID:G456346

A/Note: submitted to the EMBL/GenBank/DBJ databases by J.F. Piskurich, February 1994

R:Krajci, P.; Solberg, R.; Sandberg, M.; Oyen, O.; Jahnson, T.; Brandtzaeg, P.

Biochem. Biophys. Res. Commun. 158, 783-789, 1989

A:Title: Molecular cloning of the human transmembrane secretory component (poly-Ig recep

A/Reference number: A32263; MUID:89149795; PMID:2920039

A/Accession: A32263

A:Molecule type: mRNA

A/Residues: 72-764 <KR3>

A/Cross-references: GB:M24559; NID:G514365; PIDN:AAA36102.1; PID:G514366

R:Fallgreen-Gebauer, E.; Gebauer, W.; Bastian, A.; Kratzin, H.D.; Biffert, H.; Zimmermann

Biol. Chem. Hoppe-Seyler 374, 1023-1028, 1993

A:Title: The covalent linkage of secretory component to IgA. Structure of sIgA.

A/Reference number: S38978; MUID:94121784; PMID:8292260

A/Accession: S38978

A:Molecule type: Protein

A/Residues: 478-488; 517-526; 543-545 <FAL>

A/Note: disulfide bonds for unbound and IgA-bound forms

R:Eiffert, H.; Quantin, E.; Wiedehold, M.; Hillemeir, S.; Decker, J.; Weber, M.; Hilsch

Biol. Chem. Hoppe-Seyler 372, 119-128, 1991

A:Title: Determination of the molecular structure of the human free secretory component.

A/Reference number: S13453; MUID:91315750; PMID:1859628

A/Accession: S13453

A:Molecule type: Protein

A/Residues: 19-135; 'Q', 135-240; 'N', 235-240; 'Q', 242-261,

R:Eiffert, H.; Quantin, E.; Decker, J.; Hillemeir, S.; Hufschmidt, M.; Klingmuller, D.;

Hoppe-Seyler's Z. Physiol. Chem. 365, 1489-1495, 1984

A:Title: The primary structure of the human free secretory component and the arrangement

A/Reference number: A02112; MUID:85128981; PMID:6526384

A/Accession: A02112

A:Molecule type: Protein

A/Residues: 19-157; 'D', 159-207; 'DE', 210-228; 230-233; 'N', 235-240; 'Q', 242-261; 'Q', 263-279,

A/Note: paper in German with English abstract

C/Comment: As a 100K transmembrane receptor for polymeric immunoglobulins, secretory com

ylated, forms interchain disulfide bonds, undergoes proteolysis and transcytosis. Free s

C/Genetics:

A:Gene: GDB:PIGR

A/Cross-references: GDB:120290; OMIM:173880

A/Map position: 1q31-1q41

A:Introns: 15/1; 130/1; 349/1; 460/1; 569/1; 629/2; 670/1; 714/1; 733/3

A:Notes: the first intron occurs before the initiator codon

K:Complex: monomeric as a transmembrane receptor or free in mucosal secretions; heterode

amers; hetero-22-mer composed of one chain of secretory component, one chain of immunogl

C:Superfamily: secretory component; immunoglobulin homology

C/Keywords: duplication; glycoprotein; immunoglobulin receptor; phosphoprotein; transcyt

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-764/Product: transmembrane secretory component #status predicted <WATM>

F:19-577/Product: free secretory component #status experimental <MAT>

F:33-112/Domain: immunoglobulin homology <IM1>

F:145-222/Domain: immunoglobulin homology <IM2>

F:250-327/Domain: immunoglobulin homology <IM3>

F:364-443/Domain: immunoglobulin homology <IM4>

F:475-546/Domain: immunoglobulin homology <IM5>

F:639-661/Domain: transmembrane #status predicted <TMM>

F:662-764/Domain: intracellular #status predicted <INT>

F:40-110; 56-64; 152-220; 257-325; 271-279; 371-441; 385-395; 482-544; 496-503/Disulfide bonds:

F:83; 90; 135; 186; 421; 469; 499/Binding site: carbohydrate (Asn) (covalent) #status experime

F:486-520/Disulfide bonds: (in Ig-unbound form) #status experimental

F:486/Disulfide bonds: interchain (to IgA alpha-1 chain-192) #status experimental

F:520/Binding site: cysteine (Cys) (covalent) (in Ig-bound form) #status experimental

F:577-578/Cleavage site: Lys-Ala (unidentified proteinase) #status experimental

F:673/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 9.0%; Score 134.5; DB 1; Length 764;

. Best Local Similarity 25.3%; Pred. No. 0.0032;

Matches 64; Conservative 31; Mismatches 109; Indels 49; Gaps 9;

Qy 1 MPELLLYLLFWLSGYSTATQITGTTVNGLERGSLTVQCVY--RSGWETVLYKWCRCGAI 58

Db 1 MLFLVLTCLLAVFPATSKSPIFGPEEVNSVEGNSVITCYPPTSVNRHRTKYWCROGA 60

Qy 59 WRDCKILVKTSGEQEVKRDVRVSIKDNQNRITFTVTMBDLTKMTADTYWC--GIKTKND 116

Db 61 RGCITLISSEGVSSKYAGRANLNFPENGFFVNIAQLSQDDSGRYKCGLGINSRGLS 120

Qy 117 LGVTQVITIDPAPVTOEE-----TSSSPITLGHLDNRHKLKLSVLLPLIF--- 163

Db 121 FDVSLVSGQGLLNDTKVYVDLGRVTYINGCPFKT-ENACKRSLYKQIGLYPLVLVIDS 179

Qy 164 -----TIXLLLLVAASLLAWRMW---KYQOKAAGMSPE-----QV 195

Db 180 SGVYVNYTGRITRLDIQGTGQLLFVSVINQL--RLSDAGVLCQAGDDSNKKVADLQV 237

Qy 196 LQPLEGDLGYADL 208

Db 238 LKP-EPELYVEDL 249

RESULT 6

S48841

secretory component precursor - bovine

N:Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

K:Contains: free secretory component; transmembrane secretory component

C:Species: Bos primigenius taurus (cattle)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S48841

R:Vermeer, H.; Warmerdam, G.W.; de Boer, H.A.; Verbeet, M.P.H.

submitted to the EMBL Data Library, September 1994

A:Description: The cloning, tissue specific expression and interspecies sequence compari

A:Reference number: S48841
A:Accession: S48841
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-757 <VER>
A:Cross-references: EMBL:X81371, NID:G563340, PIDN:CAA57136.1, PID:G563341
C:Superfamily: secretory component; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin receptor; phosphoprotein; transcytosis
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-757/Product: transmembrane secretory component #status predicted <MATM>
F:19-572/Product: free secretory component #status predicted <MATF>
F:33-112/Domain: immunoglobulin homology <IM1>
F:145-222/Domain: immunoglobulin homology <IM2>
F:250-329/Domain: immunoglobulin homology <IM3>
F:363-444/Domain: immunoglobulin homology <IM4>
F:476-547/Domain: immunoglobulin homology <IM5>
F:631-653/Domain: intracellular #status predicted <TM>
F:654-757/Domain: intracellular #status predicted <INT>
F:40-110, 56-64, 152-220, 166-173, 257-324, 271-279, 370-440, 384-394, 481-543, 495-502/Disulfide
F:83, 420, 468/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:665/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 8.8%; Score 132.5; DB 1; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.0046;
Matches 59; Conservative 40; Mismatches 95; Indels 69; Gaps 8;

QY 1 MPELLTLYLLFWLSGYSYSTATOITGPTTVNGLERGSLTVQCVY--RSGWETYLKWCRCGAI 58
Db 1 MSRUFLACLLAIFPVSMKSPFGPEEVSVEGRSVSIKYYPTTSVNRHTRKWCRCQA 60

QY 59 WRDCKILYKTSGEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWC--GIEKTGND 116
Db 61 QGRCCTLLISSEGYSDVDVGRANLTNPFESGTFVVDISHLTHKDSGRYKGLGSSRGLN 120

QY 117 LGVTQVQVTDPA-----PVTEETSSPTL-----T 142
Db 121 FDVLSVSDPAQAASHAHVYTDLGRVTINCPFTRANSEKRSKSLCKKTIQDCFOVDST 180

QY 143 GHLDNRHKLKLSVL--LPLIFITXLLLVAAASLLAWRMKYQQAAGM----- 190
Db 181 GYVNSYKDRAHISILGNTLVFSVVI-----NRVKSADAGMYVCQAGDDAK 227

QY 191 -----SPQVLOPLEGDLCLYADL 208
Db 228 ADKINIDLVLEP-EPPELVYGD 249

RESULT 7
I45956
Polymeric immunoglobulin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 23-Jul-1999
C:Accession: I45956
A:Title: Cloning and characterization of two forms of bovine polymeric immunoglobulin re
A:Reference number: I45956; MUID:95186063; PMID:7880445
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-757 <KUL>
A:Cross-references: GB:L04797; NID:G388279; PIDN:AA41620.1; PID:G388280
C:Superfamily: secretory component; immunoglobulin homology
F:145-222/Domain: immunoglobulin homology <IM>

Query Match 8.8%; Score 131.5; DB 2; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.0056;
Matches 59; Conservative 39; Mismatches 96; Indels 69; Gaps 8;

QY 1 MPELLTLYLLFWLSGYSYSTATOITGPTTVNGLERGSLTVQCVY--RSGWETYLKWCRCGAI 58
Db 1 MSRUFLACLLAIFPVSMKSPFGPEEVSVEGRSVSIKYYPTTSVNRHTRKWCRCQA 60

QY 59 WEDCKILYKTSGEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWC--GIEKTGND 116
Db 61 QGRCCTLLISSEGYSDVDVGRANLTNPFESGTFVVDISHLTHKDSGRYKGLGSSRGLN 120

QY 117 LGVTQVQVTDPA-----PVTEETSSPTL-----T 142
Db 121 FDVLSVSDPAQAASHAHVYTDLGRVTINCPFTRANSEKRSKSLCKKTIQDCFOVDST 180

QY 143 GHLDNRHKLKLSVL--LPLIFITXLLLVAAASLLAWRMKYQQAAGM----- 190
Db 181 GYVNSYKDRAHISILGNTLVFSVVI-----NRVKSADAGMYVCQAGDDAK 227

QY 191 -----SPQVLOPLEGDLCLYADL 208
Db 228 ADKINIDLVLEP-EPPELVYGD 249

RESULT 8
S03421
T-cell receptor delta chain precursor (Peer) - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: S03421
A:Title: Identification and sequence of a fourth human T cell antigen receptor chain.
A:Reference number: S03421; MUID:88065901; PMID:2825032
A:Molecule type: mRNA
A:Residues: 1-232 <LOH>
A:Cross-references: EMBL:X06557; NID:G37003; PIDN:CAA29800.1; PID:G37004
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-292/Product: T-cell receptor delta chain #status predicted <MAT>

Query Match 8.6%; Score 129.5; DB 2; Length 292;
Best Local Similarity 24.3%; Pred. No. 0.0026;
Matches 35; Conservative 34; Mismatches 64; Indels 11; Gaps 4;

QY 4 LFLYLLFWLSGYSYSTATOITGPTTVNGLERGSLTVQCVYSGWETYLKWCRCGAIWRDC 62
Db 6 LFCVFAVSYSGSSVAQKVTQASSVSNPVRKAVTINCLYETISWSYIFVWKQLPSKEM 65

QY 63 KILVKTSGEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWC-----GIEKTGN 115
Db 66 IFLIQSGDEQNAKSGRYSVNFKAAKSVALTISALQLEDSAKYFCALGTGVRGLQDTDK 125

QY 116 DL-GYTVQVQVTDPAVTEETSSS 138
Db 126 LIFGKGRVTVTEPR--SQPHTKPS 147

RESULT 9
S04664
T-cell receptor delta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-May-1997
C:Accession: S04664
A:Title: Structure of the gamma/delta T cell receptor of a human thymocyte clone.
A:Reference number: S04663; MUID:89010543; PMID:2844954
A:Cross-references: EMBL:X15021
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 8.6%; Score 128.5; DB 2; Length 142;
Best Local Similarity 24.4%; Pred. No. 0.0013;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:24:14 ; Search time 24 Seconds
(without alignments)

629.181 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 1499

Sequence: 1 MPLLTLYLLFWLSGYSIAT.....SXLPGRGPBPTYSTISRP 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224.5	15.0	224	1 CM35_HUMAN	Q08708 homo sapien
2	159.5	10.6	773	1 PIGR_RABIT	P01832 cryptolagus
3	153	10.2	771	1 PIGR_MOUSE	O70570 mus musculus
4	145.5	9.7	769	1 PIGR_RAT	P15083 rattus norv
5	134.5	9.0	764	1 PIGR_HUMAN	P01833 homo sapien
6	131.5	8.8	757	1 PIGR_BOVIN	P81255 bos taurus
7	99	6.6	129	1 KV1W_HUMAN	P04431 homo sapien
8	98.5	6.6	1694	1 SN_MOUSE	Q62230 mus musculus
9	97	6.5	598	1 LIB2_HUMAN	Q8N423 h leukocyte
10	95.5	6.4	102	1 PIGR_PIG	Q29244 sus scrofa
11	92.5	6.2	506	1 SHS1_BOVIN	O46631 bos taurus
12	92.5	6.2	823	1 CEK3_CHICK	P18461 gallus gall
13	92	6.1	134	1 TVAL_RABIT	P06322 cryptolagus
14	92	6.1	249	1 HCDR_XANP2	Q56840 xanthobacte
15	92	6.1	4911	1 MLL3_HUMAN	Q8NE24 homo sapien
16	91.5	6.1	457	1 CD4_RAT	P05540 rattus norv
17	91	6.1	117	1 KV1J_HUMAN	P01602 homo sapien
18	91	6.1	650	1 LIB1_HUMAN	Q8NH16 h leukocyte
19	90	6.0	359	1 LACH_DROME	O24372 drosophila
20	89.5	6.0	116	1 HV01_HETER	P03383 heterodontu
21	88	5.9	1176	1 KML5_BOVIN	Q28824 bos taurus
22	88	5.9	4391	1 PGBM_HUMAN	P98160 homo sapien
23	87	5.8	519	1 TRPE_BUCDN	Q04697 buchnera ap
24	86.5	5.8	284	1 HCDR_HETER	Q91A17 heterodontu
25	86.5	5.8	821	1 FGR2_MOUSE	P18003 mus musculus
26	86	5.7	1141	1 CN3A_HUMAN	O14432 homo sapien
27	85.5	5.7	298	1 ERA_XYLT	Q87C05 xylella fas
28	85.5	5.7	876	1 TOPL_VIBCH	Q9KR52 vibrio chol
29	85	5.7	131	1 TVAL_HUMAN	P04436 homo sapien
30	85	5.7	3396	1 LIB4_HUMAN	P13611 homo sapien
31	84.5	5.6	448	1 LIB4_HUMAN	Q8NH16 homo sapien
32	84.5	5.6	1808	1 TENA_CHICK	P10039 gallus gall
33	84	5.6	460	1 CT54_MOUSE	Q266X5 mus musculus

ALIGNMENTS

RESULT 1

CM35_HUMAN

ID CM35_HUMAN STANDARD; PRT; 224 AA.

AC Q08708; 594 5.6 84

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE CMRF35 antigen precursor (CMRF-35).

GN CMRF35 OR CMRF35A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92249405; PubMed=1349532;

RA Jackson D.G., Hart D.N.J., Starling G., Bell J.I.;

RT "Molecular cloning of a novel member of the immunoglobulin gene

RT superfamily homologous to the polymeric immunoglobulin receptor.";

RL Eur. J. Immunol. 22:1157-1163(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21442079; PubMed=11556966;

RA Clark G.J., Cooper B., Fitzpatrick S., Green B.J., Hart D.N.;

RT "The gene encoding the immunoregulatory signaling molecule CMRF-35A

RT localized to human chromosome 17 in close proximity to other members

RT of the CMRF-35 family.";

RL Tissue Antigens 57:415-423(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,

RA Flakesley R.W., Tsuchan J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).

CC -1- TISSUE SPECIFICITY: PRESENT ON THE SURFACE OF MONOCYTES,

CC NEUTROPHILS, A PROPORTION OF PERIPHERAL BLOOD T AND B LYMPHOCYTES

CC AND LYMPHOCYTIC CELL LINES.

CC

CC


```
Qy 53 WCGAIWRDCKILVKTSGSQEVRDRVS IKDNQKNTFTVTWEDLMKTDADTYWCGIEK 112
|||
Db 61 WCREESGRCVTLASTGYTSQEVS -GRGKLTDPDKGEFVTVTDQLTQNDGSGYKCGVG 119
|||
Qy 113 TGN--DLGVTVQVITDAP---VTOEETSSPILTGHLDNRHKLKLVLLPLIFTI-- 165
|||
Db 120 NRGRLDPGVNLVSRPEPDVVKQYESTVITTCFTVATQQLKK-----SFYKVED 173
|||
Qy 166 -XLILLVAASLLAWRMKMYQKQAGMSPEQVLPQLEGDLACYADLTQLAGTSPRKATTKL 224
|||
Db 174 GELVLIDSSSKAKDPYKGR-----ITLIQISTTAKEFTVTI 212
|||
Qy 225 SSAQVDQVEVYVYVMA-----SLPKEDISYASLILGAEDQPTVCNMG 267
|||
Db 213 KHLQLNDAG-QYVCQSGSDPTAEQNVDLRLTLPGL-----LYGNLG 253
|||

RESULT 3
PIGR MOUSE
ID_PIGR_MOUSE STANDARD; PRT; 771 AA.
AC 070570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE PolymERIC-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
DE [Contains: Secretory component].
GN PIGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=95138517; PubMed=7836758;
RA Piskurich J.F., Blanchard M.H., Youngman K.R., France J.A.,
RA Kaetzel C.S.;
RT "Molecular cloning of the mouse polymeric Ig receptor. Functional
RT regions of the molecule are conserved among five mammalian species.";
RL J. Immunol. 154:1735-1747(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98072444; PubMed=9409786;
RA Martin M.G., Gutierrez E.M., Lam J.T., Li T.W.H., Wang J.;
RT "Genomic cloning and structural analysis of the murine polymeric
RT receptor (pIGR) gene and promoter region.";
RL Gene 201:189-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=99410926; PubMed=10481312;
RA de Groot N., van Kuik-Romeijn P., Lee S.H., de Boer H.A.;
RT "Over-expression of the murine polymeric immunoglobulin receptor gene
RT in the mammary gland of transgenic mice.";
RL Transgenic Res. 8:125-135(1999).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
CC TRANSMEMBRANE SEGMENT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
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DR EMBL; U06431; AAA67440.1; -.
DR EMBL; U83434; AAC53585.1; -.
DR EMBL; U83427; AAC53585.1; JOINED.
DR EMBL; U83428; AAC53585.1; JOINED.
DR EMBL; U83429; AAC53585.1; JOINED.
DR EMBL; U83430; AAC53585.1; JOINED.
DR EMBL; U83431; AAC53585.1; JOINED.
DR EMBL; U83432; AAC53585.1; JOINED.
DR EMBL; U83433; AAC53585.1; JOINED.
DR EMBL; Y16524; CAA76272.1; -.
DR EMBL; Y16525; CAA76272.1; JOINED.
DR EMBL; Y16526; CAA76272.1; JOINED.
DR EMBL; Y16527; CAA76272.1; JOINED.
DR EMBL; Y16528; CAA76272.1; JOINED.
DR EMBL; Y16529; CAA76272.1; JOINED.
DR EMBL; Y16530; CAA76272.1; JOINED.
DR EMBL; Y16531; CAA76272.1; JOINED.
DR EMBL; Y16532; CAA76272.1; JOINED.
DR MGD; MGI:103080; Pigr.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1..18
FT CHAIN 19..771
FT CHAIN 19..611
FT DOMAIN 19..645
FT TRANSMEM 646..668
FT DOMAIN 669..771
FT DOMAIN 21..120
FT DOMAIN 135..237
FT DOMAIN 245..351
FT DOMAIN 352..457
FT DOMAIN 463..563
FT DISULFID 40..110
FT DISULFID 152..220
FT DISULFID 257..324
FT DISULFID 370..440
FT DISULFID 484..546
FT CARBOHYD 90..90
FT CARBOHYD 147..147
FT CARBOHYD 170..170
FT CARBOHYD 206..206
FT CARBOHYD 420..420
FT CARBOHYD 471..471
FT CONFLICT 159..159
FT CONFLICT 396..396
FT CONFLICT 620..620
SQ SEQUENCE 771 AA; 84998 MW; 78C81302EC710730 CRC64;

Query Match 10.2%; Score 153; DB 1; Length 771;
Best Local Similarity 22.4%; Pred. No. 7.3e-06;
Matches 76; Conservative 46; Mismatches 14; Indels 74; Gaps 12;

Qy 3 LITLLALLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGMETYL-----KWCRCGA 57
|||
Db 5 LFTLLAVTF--SGVSTKSPFGQSVSIEGDSVITCYYP--DTSVNRHTRKYWCRCQ 59
|||
Qy 58 IWRDCKILVKTSGSQEVRDRVS IKDNQKRTFTVTWEDLMKTDADTYWCGIEKTDNL 117
|||
Db 60 ASGMCTTLLISNGYLSKYSGRANLINFENNTFVINIEQLTQDDTGSYKCGLGTSNRGL 119
|||
Qy 118 GYTVQVITDAP-----VTOE-----ETSSSPTLTGHH 145
|||
Db 120 SFDVSLVSVQPELPSDTHVTKDIGNVTIECPKRENAPSKSLCKKTQSCELV--- 176
|||
Qy 146 LDRHKLKLSVLLPLIF---TIXLILLVAASLLAWRMKMYQKQAGMSPE-----Q 194
|||
Db 177 IDSTEKVPNSYIGRAKLFMKGTDLTVFYVNTISHLTHNDAGLYICQAGEGPSADKKNVDLQ 236
|||
Qy 195 VLQPLEGDCYADLTQLA-----GTSPRKATTKLSSAQVDQVEVYVYVMA----- 241
|||
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Db 237 VLAP-EPELLYKDLRSSVTFECDLGREVANEAKYLCRMNKETCDVIINTLGRDPDFEGR 295
QY 242 ---LPKEDIS-YASLTGAEQDEFTYCNMGKLSXLPGRG 277
Db 296 ILITPKODNGRFSVLITGLRKEDAGHYCCGAHSSGLPQEG 335

RESULT 4
PIGR_RAT
ID PIGR_RAT STANDARD; PRT; 769 AA.
AC P15083;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
DE [Contains: Secretory component].
GN PIGR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89378226; PubMed=2776882;
RA Banting G., Brake B., Braghetta P., Luzio J.P., Stanley K.K.;
RT "Intracellular targeting signals of polymeric immunoglobulin
RL receptors are highly conserved between species.";
RL FEBS Lett. 254:177-183(1989).
CC -!- PUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
CC TRANSMEMBRANE SEGMENT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
CC
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CC
CC EMBL; X15741; CAA33758.1; -.
CC PIR; S05407; QRRTGS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC Pfam; PF00047; Ig; 5.
CC SMART; SM00409; IG; 5.
CC PROSITE; PS00835; IG LIKE; 2.
CC Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 769 POLYMERIC-IMMUNOGLOBULIN RECEPTOR.
FT CHAIN 19 611 SECRETORY COMPONENT.
FT DOMAIN 19 643 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 644 666 POTENTIAL.
FT DOMAIN 667 769 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 126 IG-LIKE V-TYPE 1.
FT DOMAIN 135 237 IG-LIKE V-TYPE 2.
FT DOMAIN 240 341 IG-LIKE V-TYPE 3.
FT DOMAIN 353 457 IG-LIKE V-TYPE 4.
FT DOMAIN 463 563 IG-LIKE V-TYPE 5.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 152 220 POTENTIAL.
FT DISULFID 257 324 POTENTIAL.
FT DISULFID 370 440 POTENTIAL.
FT DISULFID 484 546 POTENTIAL.
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 769 AA; 84798 MW; 5F849303400255A7 CRC64;

Query Match 9.7%; Score 145.5; DB 1; Length 769;
Best Local Similarity 21.4%; Pred. No. 3.5e-05;
Matches 74; Conservative 51; Mismatches 137; Indels 83; Gaps 13;

QY 4 LTYLLLLFWL-SCYSIATQITGPTTVNGLGRSLTVQCVYRSGMETYL-----KWWCRGA 57
Db 3 LSLFALLTVTFSGVSTQSPIFGPQDVSSIEGNSVITCYP---DTSVNRHTRKYWCRCQG 59
QY 58 IWRDCKILVKTSGSQEVRKRVSIKQKQKRTFTVTMEDLMKTDADYWGIEKIGNDL 117
Db 60 ANGYCATLISNGYLSKEYSGRASLINFPENSTFVINIAHLTQEDTGSYKCGLGTTNRGL 119
QY 118 GVTVOVTIDPAPVTOET-----SSSPTL-----T 142
Db 120 FFDVSLVSVQVEFPNDTHVTKDIGRTVTECRFEKGNHAKSKSLCKKRGCEBVIDS 179
QY 143 GHLDNRHK---LLKLSVLLPLFTIXLLLLVA--ASLLAWMMKYQOKAAGMSPE---- 193
Db 180 TEYVDPYSKDRALFLFKMGTSRDIFYVNIHLIPSDAGLYVQC-----AGEGPSADKN 231
QY 194 ----OVLOPLEGDLGYADLTQLA-----GTSPRKATTKLSSAQVDQVEVEVTWAS--- 241
Db 232 NADLOVLBP-EPELLYKOLRSSVTFECDLGREVANDAKYLCRKAKETCDVIINTLGRDP 290
QY 242 -----LPKEDIS-YASLTGAEQDEFTYCNMGKLSXLPGRG 277
Db 291 AFEGRILLTPRDNGRFSVLITGLRKEDAGHYCCGAHSSGLPQEG 335

RESULT 5
PIGR_HUMAN
ID PIGR_HUMAN STANDARD; PRT; 764 AA.
AC P01833;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
DE [Contains: Secretory component].
GN PIGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92039621; PubMed=1682231;
RA Krajci P., Grzeschik K.H., Geurts van Kessel A.H., Olaisen B.,
RA Brandtzaeg P.;
RT "The human transmembrane secretory component (poly-Ig receptor);
RT molecular cloning, restriction fragment length polymorphism and
RT chromosomal sublocalization.";
RL Hum. Genet. 87:642-648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92387236; PubMed=1355431;
RA Krajci P., Kvale D., Tasken K., Brandtzaeg P.;
RT "Molecular cloning and exon-intron mapping of the gene encoding human
RT transmembrane secretory component (the poly-Ig receptor).";
RL Eur. J. Immunol. 22:2309-2315(1992).
RN [3]
RP SEQUENCE OF 72-764 FROM N.A.
RX MEDLINE=89149795; PubMed=2920039;
RA Krajci P., Solberg R., Sandberg M., Oyen O., Jahnsen T.,
RA Brandtzaeg P.;
RT "Molecular cloning of the human transmembrane secretory component
RT (poly-Ig receptor) and its mRNA expression in human tissues.";
RL Biochem. Biophys. Res. Commun. 158:783-789(1989).
RN [4]
RP SEQUENCE OF 19-577, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

```


[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Mammary gland, and Small intestine;
RX MEDLINE=95186063; PubMed=7880445;
RA Kulseth M.A., Krajci P., Myklebost O., Rognes S.,
RT "Cloning and characterization of two forms of bovine polymorphic
RL immunoglobulin receptor cDNA.";
RL Gene 164:329-333(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96069604; PubMed=7590352;
RA Verbeet M.P., Vermeer H., Warner G.C., de Boer H.A., Lee S.H.;
RT "Cloning and characterization of the bovine polymorphic immunoglobulin
RL receptor-encoding cDNA.";
RL Gene 164:329-333(1995).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
CC TRANSMEMBRANE SEGMENT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=long;
CC IsoId=P81265-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P81265-2; Sequence=VSP 002547;
CC -!- TISSUE SPECIFICITY: FOUND IN MAMMARY GLAND, JEJUNUM, LUNG, KIDNEY
CC AND SMALL INTESTINE.
CC -!- PTM: IN THE ABSENCE OF DIMERIC IGA, SER-727 IS PHOSPHORYLATED
CC WHICH ALLOWS PIGR TO FUNCTION NORMALLY
CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
CC
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CC
CC EMBL; L04797; AAC41620.1; -;
CC DR EMBL; X81371; CAA57136.1; -;
CC DR PIR; I45956; I45956.
CC DR PIR; S48841; S48841.
CC DR InterPro; IPR007110; IG-like.
CC DR Pfam; PF00047; Ig; 5.
CC DR SMART; SM00409; IG; 3.
CC DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal;
KW Polymorphism; phosphorylation; Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 757
FT CHAIN 19 599
FT CHAIN 19 632
FT DOMAIN 633 653
FT TRANSMEM 654 757
FT DOMAIN 145 126
FT DOMAIN 145 237
FT DOMAIN 250 341
FT DOMAIN 353 457
FT DOMAIN 461 560
FT DOMAIN 40 110
FT DISULFID 56 64
FT DISULFID 152 220
FT DISULFID 257 324
FT DISULFID 271 279
FT DISULFID 370 440
FT DISULFID 384 394
FT DISULFID 481 543

FT DISULFID 485 519 BY SIMILARITY.
FT DISULFID 495 502
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 727 727 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPLIC 129 346 Missing (in isoform Short).
FT FTID=VSP_002547.
FT VARIANT 29 29 T -> S.
FT VARIANT 142 142 V -> I.
FT VARIANT 404 404 I -> M.
FT VARIANT 413 413 A -> V.
FT VARIANT 435 435 T -> A.
SQ SEQUENCE 757 AA; 82434 MW; DCED67DD6A6E6C6 CRC64;
Query Match 8.8%; Score 131.5; DB 1; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.00063;
Matches 59; Conservative 39; Mismatches 96; Indels 69; Gaps 8;
QY 1 MPLLLYLLFWLSGYSIATQITGTTVNGLESGSLTVQCVY--RSGWETYLKMWCRGAI 58
DB 1 MSRLFLACLLAIFPVVSMKSPIFGPEEVSVEGRSVSKICYPPPTSVNRHTRKYWCRGA 60
QY 59 WRDCILVKTSGEQEVKRDVRSIKDNQKRTFTVTMEDLMKTDADTYWC--GIEKTGND 116
DB 61 QGRCITLISSEGVSDDYVGRANLNFPESTGFVVDISHLTHKDSGRYKCGLGISRGIN 120
QY 117 LGVTQVITDPA-----PVTQETSSPTL-----T 142
DB 121 FDSLEVSQDPAQASHAHVYVDLGRVTYINCPTFRANSEKRSKCKTIQDCFQVWDST 180
QY 143 GHLDNRHKLKLSVL--LPLFTIXLLLVAAASLLAWRMKYQQAAGM----- 190
DB 181 GVVSNSYKDRAHISILGNTLWFSVI-----NRVLSLDAGMYVCQAGDDAK 227
QY 191 -----SPQVQPLEGDLCYADL 208
DB 228 ADKINIDQLVLEP-EPFLVYGD 249
RESULT 7
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-I region Walker precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Kiebeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
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CC
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC PIR; A01883; KIHUNK.
CC HSSP; P01607; 1REI.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC

DR PIR: S50065; S50065.
 DR PDB; 1QFO; 16-APR-99.
 DR DR MGD; MGI:99668; Sn.
 DR GO; GO:0016021; C: integral to membrane; ISS.
 DR GO; GO:0005539; F: sugar binding; ISS.
 DR GO; GO:0016337; P: cell-cell adhesion; ISS.
 DR GO; GO:0007160; P: cell-matrix adhesion; ISS.
 DR GO; GO:0006934; P: inflammatory response; ISS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig: 16.
 DR SMART; SM00408; IGC2; 5.
 DR PROSITE; PS00835; IG_LIKE; 14.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
 Immunoglobulin domain; Repeat; Alternative splicing; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 1694
 FT DOMAIN 20 1638
 FT TRANSMEM 1639 1659
 FT DOMAIN 1660 1694
 FT DOMAIN 20 136
 FT DOMAIN 153 235
 FT DOMAIN 239 321
 FT DOMAIN 326 406
 FT DOMAIN 416 508
 FT DOMAIN 509 594
 FT DOMAIN 602 701
 FT DOMAIN 704 781
 FT DOMAIN 795 890
 FT DOMAIN 894 972
 FT DOMAIN 979 1078
 FT DOMAIN 1080 1160
 FT DOMAIN 1171 1263
 FT DOMAIN 1244 1336
 FT DOMAIN 1341 1438
 FT DOMAIN 1441 1519
 FT DOMAIN 1533 1626
 FT SITE 827 829
 FT DISULFID 36 166
 FT DISULFID 41 98
 FT DISULFID 160 218
 FT DISULFID 263 306
 FT DISULFID 347 391
 FT DISULFID 434 492
 FT DISULFID 532 576
 FT DISULFID 625 685
 FT DISULFID 725 770
 FT DISULFID 813 872
 FT DISULFID 911 955
 FT DISULFID 1000 1062
 FT DISULFID 1102 1144
 FT DISULFID 1188 1236
 FT DISULFID 1276 1319
 FT DISULFID 1362 1421
 FT DISULFID 1462 1508
 FT DISULFID 1551 1610
 FT CARBOHYD 159 159
 FT CARBOHYD 266 266
 FT CARBOHYD 299 299
 FT CARBOHYD 340 340
 FT CARBOHYD 500 500
 FT CARBOHYD 583 583
 FT CARBOHYD 693 693
 FT CARBOHYD 722 722
 FT CARBOHYD 737 737
 FT CARBOHYD 882 882
 FT CARBOHYD 1089 1089
 FT CARBOHYD 1099 1099
 FT CARBOHYD 1246 1246
 FT CARBOHYD 1459 1459

FT CARBOHYD 1473 1473 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 326 340 MAEVMNPGVPLEN -> SESWMRLRGVSGKH (in isoform 2).
 FT VARSPLIC 341 1694 /FTID=VSP 002573.
 FT VARSPLIC 1528 1598 Missing (in isoform 2).
 FT VARSPLIC 1528 1598 /FTID=VSP 002574.
 FT VARSPLIC 1528 1598 YPKPTLIVFVEPQGGHGLDQVSEPLAILTLHRGSG
 FT VARSPLIC 1528 1598 LVANSLHDTAPKPHIRVTAPNALRVIE -> CEYEPIS
 FT VARSPLIC 1528 1598 ALCLSLHDTGVPQAFSSAQSGFKGRLTLASSLAGQWVF
 FT VARSPLIC 1528 1598 VSMGLGPAKWRLLLPFWDEYER (in isoform 3).
 FT VARSPLIC 1528 1598 /FTID=VSP 002575.
 FT VARSPLIC 1528 1598 Missing (in isoform 3).
 FT MUTAGEN 21 21 /FTID=VSP 002576.
 FT MUTAGEN 116 116 W->Q: LOSS OF SIALIC ACID BINDING.
 FT MUTAGEN 116 116 R->A: LOSS OF SIALIC ACID BINDING.
 FT MUTAGEN 116 116 R->L: 10-FOLD LOSS IN AFFINITY TO SIALIC
 Query Match 6.6%; Score 98.5; DB 1; Length 1694;
 Best Local Similarity 23.2%; Pred. No. 1.7;
 Matches 39; Conservative 22; Mismatches 56; Indels 51; Gaps 8;
 QY 3 LTLTYLLFWLSCYSIATQ---ITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCG--A 57
 DB 1 MCVLSLLLASVFLSGQTWCVSPKXVQGLSGCLLIPCLFSYPADVPVS---NGITA 57
 QY 58 IWRDCKILVKTSGSEQEV-----XRDVSIKDNQKNRTFTVTMEDLMKTDADT 105
 DB 58 IW-----YYDSGKRQVVIHSGDPKLVKDRFRGAEALMGNDHKVCLLLKDLKPEDSGT 112
 QY 106 Y-----WCGIEKTGNDLGVTVQVTDPAVPTQETSSSTLT 142
 DB 113 YNFRFISDSNRWLDVK-----GTVTVTTDPS-----FTIT 145
 RESULT 9
 LIB2 HUMAN STANDARD; PRT; 598 AA.
 ID Q8N423; O75017; Q8NHJ7; Q8NHJ8;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor subfamily B member 2 precursor
 DE (leukocyte immunoglobulin-like receptor 2) (LIR-2) (immunoglobulin-
 DE like transcript 4) (ILT-4) (Monocyte/macrophage immunoglobulin-like
 DE receptor 10) (MIR-10) (CD85d antigen).
 GN LILRB2 OR LIR2 OR ILT4 OR MIR10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND FUNCTION.
 RC TISSUE=Dendritic cell, and Peripheral blood monocytes;
 RX MEDLINE=98208234; PubMed=9548455;
 RA Borges L., Hsu M.-L., Fanger N., Rubin M., Cosman D.;
 RT "A family of human lymphoid and myeloid Ig-like receptors, some of
 RT which bind to MHC class I molecules.";
 RL J. Immunol. 159:5192-5196(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-161; HIS-300
 RP AND CYS-306.
 RL Canavez F.C.;
 RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Peripheral blood leukocytes;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,


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QY 84 DNQNRRTFTVTMEDLMKTDADTYWC-----GIEKTGNDLGVTQVTTI 125
Db 373 EYPKYQA-EFFPMSFVTSAAHGYRCYCSLNSDPYLLSHPSPELVVSGPMSGSS----- 426
QY 126 DPAPVQTEETSSP-----TLTGHLDN---RHKLKLSVLLPLIFTXILLVAASLLA 177
Db 427 -PPPTGPSTPAGPDPQLPTGSDPQSGGLRHGLVWIGILVAVVLLLLLLLLLLFLILRH 485
QY 178 WRMMK-----YQKAAGMSPEQVLQPLE-----GDLCVADLTQLAGTSPRKAT 221
Db 486 RQGHKHTSTORKADQFQHPAGAVGEPTDRGLQWRSSPADAQENLYAAVKOTQPE--- 542
QY 222 TKLSSAQVDQVEVYVTTWASLPKEDISYA-----SUTLGAEDQEPYCNNGKLSXLPGR-- 276
Db 543 -----DGVEMDTRAAASAPQDVTYAQLHSLTLRKATEPP-----PSQER 583
QY 277 -GPPEPTYSIIS 288
Db 584 EPPAEPSIYATLA 596

RESULT 10
PIGR FIG
ID FIGR FIG STANDARD; PRT; 102 AA.
AC Q29244;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-OCT-2003 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor (Poly-Ig receptor) (PIGR)
DE (Fragment).
GN PIGR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -----
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CC -----
CC EMBL; F14851; CAA23294.1; -
CC InterPro; IPR007110; IG-LIKE.
CC PROSITE; PS50835; IG_LIKE; PARTIAL.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein.
FT NON TER 1
FT NON TER 102 102
SQ SEQUENCE 102 AA; 11205 MW; 82C915264B1508E8 CRC64;

Query Match 6.4%; Score 95.5; DB 1; Length 102;
Best Local Similarity 26.7%; Pred. No. 0.083;
Matches 24; Conservative 16; Mismatches 49; Indels 1; Gaps 1;

QY 25 FTTVNGLRGSLTVQCVYRSQWETYLKWCRCGAIWRDCKILVTSQSEQVYKRDVSIKD 84
Db 9 PELIYGLRGSVTFDCALGQEMANVAKFLCQLKNGKTCNVVINTLGGKAQDFEGRILLTP 68
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```
QY 85 NQNRRTFTVTMEDLMKTDADTYWCIEKGTG 114
Db 69 -KENGHSFVHTGLRKEDAGHYLCGXHPDG 97

RESULT 11
SHSL_BOVIN
ID SHSL_BOVIN STANDARD; PRT; 506 AA.
AC O46631; O46632;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHL substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (Sirp-alpha-1) (Myp-1 antigen).
GN PTPNS1 OR SHPS1 OR SIRP OR MYD1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.; AND VARIANTS SER-23; ALA-28; LEU-61; ARG-70;
RP HIS-120; 125-GLN; 129-GLY; 129-HIS; 132-VAL; ASN-145; VAL-153;
RP ASP-203; ARG-261; LEU-302; LEU-316; ARG-337; ASN-367; LEU-422; PHE-429
RP AND GLU-433.
RC STRAIN=Frison; TISSUE=Peripheral blood;
RX MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells."
RL Eur. J. Immunol. 28:1-11(1998).
CC -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6,
CC PTPN11 and other binding partners from the cytosol to the
CC plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC outgrowth and glial cell attachment. May play a key role in
CC intracellular signaling during synaptogenesis and in synaptic
CC function. Involved in the negative regulation of
CC receptor tyrosine kinase-coupled cellular responses induced by
CC cell adhesion, growth factors or insulin. Mediates negative
CC regulation of phagocytosis, mast cell activation and dendritic
CC cell activation. CD47 binding prevents maturation of immature
CC dendritic cells and inhibits cytokine production by mature
CC dendritic cells (By similarity).
CC -!- SUBUNIT: binds PTPN11 when tyrosine-phosphorylated, except in
CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC Binds JAK2 irrespective of its phosphorylation status and forms a
CC stable complex. Binds SCAP1 and/or SCAP2. The resulting complex
CC recruits FVB. Binds FGR and PTK2B (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen macrophages.
CC Detected in skin dendritic cells.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y11045; CAA71942.1; -
CC EMBL; Y11046; CAA71943.1; -
CC InterPro; IPR007110; IG-LIKE.
CC InterPro; IPR003597; IG_C1.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; ig; 3.
```


KW Repeat; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 823
 FT DOMAIN 24 379
 FT TRANSMEM 380 400
 FT DOMAIN 401 823
 FT DOMAIN 42 128
 FT DOMAIN 156 249
 FT DOMAIN 258 360
 FT DOMAIN 135 145
 FT DOMAIN 483 772
 FT NP BIND 489 497
 FT BINDING 519 519
 FT ACT SITE 628 628
 FT MOD RES 659 659
 FT DISULFID 65 110
 FT DISULFID 181 233
 FT DISULFID 280 344
 FT CARBOHYD 86 86
 FT CARBOHYD 126 126
 FT CARBOHYD 148 148
 FT CARBOHYD 230 230
 FT CARBOHYD 243 243
 FT CARBOHYD 267 267
 FT CARBOHYD 299 299
 FT CARBOHYD 320 320
 FT CARBOHYD 333 333
 SQ SEQUENCE 823 AA; 92299 MW; 42BF3CC4EA02FD43 CRC64;

Query Match 6.2%; Score 92.5; DB 1; Length 823;
 Best Local Similarity 21.6%; Pred. No. 2.4;
 Matches 58; Conservative 41; Mismatches 86; Indels 83; Gaps 13;

QY 25 PTTVNGLESLTQVYRSGWETYLKWCRCGAIWRDCKILVKTSGSE-----QEV 75
 Db 265 PANASAVVGVDVEFCVKYVSDAOPHIQWIKH-----VERNGSKYGDGLPYLQVL 314
 QY 76 KDRVSIKDNQ-----KNRFTVTMEDLMKTDADTYWCGIEKTDGLV---TVQVTD 126
 Db 315 KAAGVNTDKIEVLVIRNVTF-----EDAGEYTC---LAGNSIGISFHTAMLTVL 362
 QY 127 PAPVTOERTSSPTLTGHLDNRKLLKLSVLLPLFTLXLLLVAAASLLAWRMKYOQK 186
 Db 363 PAPEKEKEFTSP-----DYLEIAICYGVFLACWL---TVLCRKQNTTK 408
 QY 187 AAGMSPEQVLOPLEGDL-----CYADLTQLAGTSR-KATKLS-----A 227
 Db 409 -----PDPSSQPAVHKLTKRIPLRQVTVSADSSSMNSNTPLVTRITLSSTADAPMLA 463
 QY 228 QVDOVEVEVVTMASLPKEDISYASLTIG 255
 Db 464 GVSEVE-----LPEDPKWEFFRDKLTIG 486

RESULT 13
 ID TVAI RABIT STANDARD; PRT; 134 AA.
 AC P06322;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE T-cell receptor alpha chain V region RL-5 precursor.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177569; PubMed=3485798;
 RA Marche P.N., Kindt T.J.;
 RT "Two distinct T-cell receptor alpha-chain transcripts in a rabbit
 T-cell line: implications for allelic exclusion in T cells."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2190-2194 (1986).

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M12885; AAA11469.1; --
 DR PIR; A02013; RWRBAY.
 DR HSSP; P01607; LREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003599; IG.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134
 FT CHAIN 21 134
 FT DOMAIN 21 114
 FT DOMAIN 115 134
 FT CARBOHYD 134 134
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14856 MW; A29F3F8570BEE15E CRC64;
 Query Match 6.1%; Score 92; DB 1; Length 134;
 Best Local Similarity 20.9%; Pred. No. 0.24;
 Matches 28; Conservative 39; Mismatches 55; Indels 12; Gaps 5;

QY 4 LFLYLLLLFWL---SGYSIATQITGPTVNGLESLTQVYRSGWETYLKWCRCGAIWR 60
 Db 8 VTVVLLITVTRTNGASV-TQTEGPVILS--EGSSLTLNLCNYQTSYSGFLFWYVQ-YLHE 63
 QY 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLV 120
 Db 64 GQQLLOSTENQORVHOGFHATFVKDSSPHLHKSSQLSDSAVYCALRR-----GAS 118
 QY 121 VQVITDPAVPTQEE 134
 Db 119 NKLTGLTGTLKVE 132

RESULT 14
 ID HCDR_XAMP2 STANDARD; PRT; 249 AA.
 AC Q56840;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 2-(R)-hydroxypropyl-CoM dehydrogenase (EC 1.1.1.268).
 OS Xanthobacter sp. (strain Py2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 OX NCBI_TaxID=78245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95219103; PubMed=7704278;
 RA Swaving J., Weijers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;
 RT "Complementation of Xanthobacter Py2 mutants in epoxyalkane
 degradation: expression and nucleotide sequence of the complementing
 DNA fragment."
 RL Microbiology 141:477-484 (1995).
 RN [2]
 RP SEQUENCE OF 1-10, AND CHARACTERIZATION.
 RX MEDLINE=98070376; PubMed=9405410;
 RA Allen J.R., Ensign S.A.;
 RT "Purification to homogeneity and reconstitution of the individual
 components of the epoxide carboxylase multi-protein enzyme complex
 from Xanthobacter strain Py2."
 RL J. Biol. Chem. 272:32121-32128 (1997).
 CC -!- FUNCTION: Catalyzes the oxidation of 2-(R)-hydroxyalkyl thioesters

RA Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee Y.C.,
 RT Lee J.W.;
 RT "Activating signal cointegrator 2 belongs to a novel steady-state
 RL Mol. Cell. Biol. 23:140-149(2003).
 CC -!- FUNCTION: Belongs to the ASC-2/NCOA6 complex (ASCOM), a
 CC coactivator complex of nuclear receptors, involved in
 CC transcriptional coactivation. MLL3 may be a catalytic subunit of
 CC this complex, which weakly methylates lys-4 of histone H3. This is
 CC a specific tag for epigenetic transcriptional activation. May be
 CC involved in leukemogenesis and developmental disorder.
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine =
 CC S-adenosyl-L-homocysteine + histone N(6)-methyl-L-lysine.
 CC -!- SUBUNIT: Belongs to the ASC-2/NCOA6 complex (ASCOM), which
 CC contains ASC-2/NCOA6, the retinoblastoma-binding protein RBQ-3/
 CC RBP5, alpha- and beta-tubulins, the trithorax group proteins
 CC MLL2 and MLL3, and ASH2/ASCL2. Interacts with histone H3.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8NEZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8NEZ4-2; Sequence=VSP_008561, VSP_008562;
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and ovary, followed
 CC by brain and liver. Also expressed in placenta, peripheral
 CC blood, fetal thymus, heart, lung and kidney. Within brain,
 CC expression was highest in hippocampus, caudate nucleus and
 CC substantia nigra. Not detected in skeletal muscle and fetal liver.
 CC -!- DOMAIN: The SET domain interacts with histone H3 but not H2A, H2B
 CC and H4, and may have a H3 lysine specific methylation activity.
 CC -!- MISCELLANEOUS: Found in a critical region of chromosome 7, which
 CC is commonly deleted in malignant myeloid disorders. Partial
 CC duplication of the MLL3 gene are found in the juxtacentromeric
 CC region of chromosomes 1, 2, 13 and 21. Juxtacentromeric
 CC reshuffling of the MLL3 gene has generated the BAGE genes.
 CC -!- SIMILARITY: Belongs to the TRX/MLL family.
 CC -!- SIMILARITY: Contains 1 DHHC-type zinc finger.
 CC -!- SIMILARITY: Contains 6 PHD-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 post-SET domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- SIMILARITY: Contains 1 SET domain.
 CC -----
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 CC -----
 DR EMBL; AY024361; AAK00583.1; -;
 DR EMBL; AF264750; AAF74766.2; -;
 DR EMBL; AC006017; AAD45822.1; -;
 DR EMBL; AC104692; -; NOT ANNOTATED CDS.
 DR EMBL; AC005631; -; NOT ANNOTATED_CDS.
 DR EMBL; AB040939; BAAS6030.2; -;
 DR EMBL; AK022687; BAB14179.1; -;
 DR EMBL; AK075113; BAC11409.1; -;
 DR EMBL; AL833924; CAD38780.1; -;
 DR EMBL; HGNC:13726; MLL3.
 DR MIM; 606833; -;
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR003889; Fyric_C.
 DR InterPro; IPR003888; Fyric_N.
 DR InterPro; IPR000910; HMG_12_box.
 DR InterPro; IPR003616; PostSET.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR001594; Znf_DHHC.
 DR InterPro; IPR001965; Znf_PHD.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00505; HMG_box; 1.
 DR Pfam; PF00628; PHD; 6.

DR Pfam; PF00856; SET; 1.
 DR SMART; SM00542; FYRC; 1.
 DR SMART; SM00541; FYRN; 1.
 DR SMART; SM00398; HMG; 1.
 DR SMART; SM00249; PHD; 8.
 DR SMART; SM00508; PostSET; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00868; POST_SET; 1.
 DR PROSITE; PS0280; SET; 1.
 DR PROSITE; PS0216; ZF_DHHC; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 5.
 DR PROSITE; PS00016; ZF_PHD_2; 6.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Transferase; Methyltransferase; Chromatin regulator; Activator;
 KW DNA-binding; Nuclear protein; Transcription regulation; Coiled coil;
 KW Zinc-finger; Repeat; Alternative splicing; Polymorphism.
 FT ZN_FING 341..391
 FT ZN_FING 344..389
 FT ZN_FING 348..438
 FT ZN_FING 436..489
 FT ZN_FING 464..520
 FT ZN_FING 957..1010
 FT ZN_FING 1007..1057
 FT ZN_FING 1084..1139
 FT DOMAIN 4770..4891
 FT DOMAIN 4895..4911
 FT DOMAIN 92..112
 FT DOMAIN 644..672
 FT DOMAIN 1338..1366
 FT DOMAIN 1754..1787
 FT DOMAIN 3054..3081
 FT DOMAIN 3173..3272
 FT DOMAIN 3331..3433
 FT DNA_BIND 34..46
 FT DOMAIN 1719..1796
 FT DOMAIN 1834..2281
 FT DOMAIN 2412..2630
 FT DOMAIN 2690..2786
 Query Match 6.1%; Score 92; DB 1; Length 4911;
 Best Local Similarity 25.3%; Pred. No. 27;
 Matches 59; Conservative 32; Mismatches 84; Indels 58; Gaps 13;
 QY 86 QKQRTFTVMDLMDKTDADTYWCG-----IEKGNLDGVTVQVTI-----DPAP 129
 DB 616 EKQISNEVDSEDLKMSSEVGHICGEDQIEDKVEVTEVTVTHQITVQEQQLLEPEP 675
 QY 130 VTQETSSPTTGHLDNRKLLKLSVLLPLFTI-----XLLLLVAASLLAWRM-KY 183
 DB 676 VVRSERPP-----KLNVSVTLPLETVSPHEESISLCPEEQVIERLQGEK 724
 QY 184 QOK-----AAGMSPEQVLPLEGDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVT 238
 DB 725 EKENSELSTGLMDSEMTPTIEG--CVKDSVQ-GGKS-----IKLSS-----ETESSFSS 772
 QY 239 MASLPKEDISYA---SLTLGAEDQPTCYNMGXLSXLPGRGPPEPEYETIS 288
 DB 773 SADISKADVSSSPPTSSDPLPSHMLHNY--PSALSS-----SAGNIMPTIISVT 820
 Search completed: September 16, 2004, 12:37:46
 Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:35:20 ; Search time 32 Seconds
(without alignments)
467.860 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPLLTYLLFLWLSGVSIAT.....SXLPGRGPEPTVSTISRP 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCURS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	451.5	30.1	201	3	US-08-955-937A-2
2	451.5	30.1	201	3	US-09-300-985-2
3	434	29.0	195	3	US-08-955-937A-4
4	434	29.0	195	3	US-09-300-985-4
5	329.5	22.0	298	4	US-09-582-934-2
6	323	21.5	301	4	US-09-582-934-1
7	197.5	13.2	164	4	US-09-582-934-3
8	189.5	10.6	624	2	US-08-642-406A-22
9	159.5	10.6	624	4	US-09-199-534-22
10	159.5	10.6	624	4	US-09-199-534-22
11	159.5	10.6	773	3	US-08-434-000A-2
12	159.5	10.6	773	3	US-09-312-157-2
13	153	10.2	771	3	US-08-434-000A-8
14	153	10.2	771	4	US-09-312-157-8
15	145.5	9.7	769	3	US-08-434-000A-10
16	145.5	9.7	769	4	US-09-312-157-10
17	134.5	9.0	608	4	US-09-095-385-4
18	133.5	8.9	746	3	US-08-434-000A-4
19	133.5	8.9	746	4	US-09-312-157-4
20	132.5	8.8	757	3	US-08-434-000A-6
21	132.5	8.8	757	4	US-09-312-157-6
22	127.5	8.5	294	6	S260223-1
23	125	8.3	303	3	US-08-985-950-2
24	125	8.3	303	4	US-09-546-049-2
25	121.5	8.1	334	4	US-09-197-970B-7
26	113.5	7.6	230	4	US-09-148-545-214
27	113.5	7.6	231	4	US-09-148-545-215

28	111	7.4	109	3	US-08-961-564A-9	Sequence 9, Appli
29	107	7.1	46	3	US-08-955-937A-12	Sequence 12, Appl
30	107	7.1	46	3	US-09-300-985-12	Sequence 12, Appl
31	105	7.0	451	1	US-08-287-001A-2	Sequence 2, Appli
32	105	7.0	451	5	PCT-US95-09941-2	Sequence 2, Appli
33	100	6.7	307	4	US-09-197-970B-3	Sequence 3, Appli
34	99	6.6	128	4	US-09-450-520A-6	Sequence 6, Appli
35	97	6.5	598	4	US-09-310-463-10	Sequence 10, Appl
36	97	6.5	598	4	US-08-842-448A-10	Sequence 10, Appl
37	97	6.5	615	3	US-08-985-950-16	Sequence 16, Appl
38	97	6.5	615	3	US-08-985-950-18	Sequence 18, Appl
39	97	6.5	615	4	US-09-546-049-18	Sequence 18, Appl
40	97	6.5	615	4	US-09-546-049-18	Sequence 4, Appli
41	95.5	6.4	255	2	US-07-690-192-4	Sequence 4, Appli
42	94	6.3	128	2	US-08-470-139-26	Sequence 26, Appl
43	94	6.3	128	4	US-09-347-061-26	Sequence 26, Appl
44	93.5	6.2	165	4	US-09-148-545-149	Sequence 149, App
45	93	6.2	241	2	US-07-916-098A-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-08-955-937A-2
; Sequence 2, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUIJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-955-937A-2

Query Match 30.1%; Score 451.5; DB 3; Length 201;
Best Local Similarity 49.8%; Pred. No. 1.1e-38;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;


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QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLSG---CFSIQGPESVRAPEQGSGLTVQCHYKQGWETIYIKWCRCGVWRDTCILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVRDRVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSQGEKSDRVSIKQKQKRTFTVTMEGLRRDADVYWCGERGPDGLGTQVKVIVDP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTOEETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 EGAA-STTASPTNSNMAVFGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-----QPLEGD 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      173 KGSQVPEEPGEQPIYMFSEPLTKDM 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 2

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US-09-300-985-2
; Sequence 2, Application US/09300985A
; Patent No. 6232441

```

GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSSEG
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 201
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-300-985-2

```

```

Query Match      30.1%; Score 451.5; DB 3; Length 201;
Best Local Similarity 49.8%; Pred. No. 1.1e-38;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;

QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLSG---CFSIQGPESVRAPEQGSGLTVQCHYKQGWETIYIKWCRCGVWRDTCILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVRDRVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSQGEKSDRVSIKQKQKRTFTVTMEGLRRDADVYWCGERGPDGLGTQVKVIVDP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTOEETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 EGAA-STTASPTNSNMAVFGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-----QPLEGD 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      173 KGSQVPEEPGEQPIYMFSEPLTKDM 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 3

```

US-08-955-937A-4
; Sequence 4, Application US/08955937A
; Patent No. 6020161

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GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSSEG

```

```

; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-937A-4

```

```

Query Match      29.0%; Score 434; DB 3; Length 195;
Best Local Similarity 49.5%; Pred. No. 6.5e-37;
Matches 100; Conservative 21; Mismatches 57; Indels 24; Gaps 8;

QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLSG---CFSIQGPESVRAPEQGSGLTVQCHYKQGWETIYIKWCRCGVWRDTCILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVRDRVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSQGEKSDRVSIKQKQKRTFTVTMEGLRRDADVYWCGERGPDGLGTQVKIDCXP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTOEETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 RGSQFPQQSSPTNSNMAVFGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 173
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-QPLEGD 202
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      174 KGSQVPEEPGEQPIYMFSEPLTKDM 191
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 4

```

US-09-300-985-4
; Sequence 4, Application US/09300985A
; Patent No. 6232441

```

GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSSEG
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A

```

; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (122) (170) (184)
US-09-300-985-4

Query Match 29.0%; Score 434; DB 3; Length 195;
Best Local Similarity 49.5%; Pred. No. 6.5e-37;
Matches 100; Conservative 21; Mismatches 57; Indels 24; Gaps 8;
QY 8 LLLFWLSGYSIATQITGPTTWNGLRGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILYK 67
DB 7 LLLLSLGG---CFSIQGPESVRAPEQSLTVQCHYKQGWETYLKWCRCGVRMDTCKILIE 63
QY 68 TSGSEQEVKEDRVSIKDNOKNRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVTIDP 127
DB 64 TRGSEQEKSDRVSIKDNOKRTFTVTMEGLRDDADVYWCGIERGPDGLGTQVKIDCRP 123
QY 128 APVTQBTSSPT-----LTGHLDNRHKLKLSVLLPLIFITXILLLVAASLLAWRM 181
DB 124 RGSFPQQSQSSPNSNMAVIGSHKRN-HYMLLVFKVPI-----LLILVNXLL--W--L 173
QY 182 KYQQKAAGMSPEQVL-QPLEGD 202
DB 174 KGSQRV-----PEEPXEQPIYMD 191

RESULT 5
US-09-582-934-2
; Sequence 2, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-2

Query Match 22.0%; Score 329.5; DB 4; Length 298;
Best Local Similarity 32.9%; Pred. No. 8.1e-26;
Matches 105; Conservative 51; Mismatches 98; Indels 65; Gaps 15;
QY 8 LLLFWLSG---YSIATQITGPTTWNGLRGSLTVQCVYRSGWETYLKWCRCGAIWRDCKI 64
DB 7 LLLIWPQCFALSKCRTVAGPW-----GSLSVQCPYEKEHRTLKNYKWRCPPIFLCDK 59
QY 65 LVKTSQEQVKRDRVSIKDNOKNRTFTVTMEDLMKTDADTYWCGIE---KTGNDLGV 120
DB 60 IVETKGSACK-RNGRVSRDSPANLSFTVLTLENLTEDAGTYWCGVDTPLWRDHPDPVE 118

Query Match 21.5%; Score 323; DB 4; Length 301;
Best Local Similarity 32.9%; Pred. No. 3.8e-25;
Matches 106; Conservative 51; Mismatches 97; Indels 68; Gaps 16;
QY 8 LLLFWLSG---YSIATQITGPTTWNGLRGSLTVQCVYRSGWETYLKWCRCGAIWRDCKI 64
DB 7 LLLIWPQCFALSKCRTVAGPW-----GSLSVQCPYEKEHRTLKNYKWRCPPIFLCDK 59
QY 65 LVKTSQEQVKRDRVSIKDNOKNRTFTVTMEDLMKTDADTYWCGIE---KTGNDLGV 120
DB 60 IVETKGSACK-RNGRVSRDSPANLSFTVLTLENLTEDAGTYWCGVDTPLWRDHPDPVE 118

```
US-09-582-934-3
; Sequence 3, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582.934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/N299/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-3

Query Match      13.2%; Score 197.5; DB 4; Length 164;
Best Local Similarity 36.9%; Pred. No. 1.5e-12;
Matches 48; Conservative 23; Mismatches 40; Indels 19; Gaps 4;

QY 22 ITGTTVNGLRGSLTVQCVYRSGWETVYKWCRCGAIWRCKILVKTSGSEQEVRDRVS 81
DB 11 VAGPW-----GSLSVQCPVEKEHRTLNKWCRCPPQIFLCKIVETKGSAGK-RNGRVS 62

QY 82 IKDNQKRTFTVTMEDLMKTDADTYWCGIE-----KTGNDLGVTQVTI-----PPAPV 130
DB 63 IRDSPANLSFTVLTLENLTEDAGTYWCGVDTFWLURDFHPVVEVSVFPASTSMTPASI 122

QY 131 TQETSSSPT 140
DB 123 TAAKTSITT 132

RESULT 8
US-08-642-406A-22
; Sequence 22, Application US/08642406A
; Patent No. 5959177
; GENERAL INFORMATION:
; APPLICANT: Hein, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; TITLE OF INVENTION: SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5959177th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642.406A
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/591,823
; FILING DATE: 02-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/427,765

US-09-582-934-3
; FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 184.2
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-406A-22

Query Match      10.6%; Score 159.5; DB 2; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTYLLFLWLSGYSTAT-----QITGPTVNGLRGSLTVQCVYRSGWET--YIKW 52
DB 1 MALFLITCLLAVFSAAQSSLLGPSIFGPEVNVLEGSVITCYYPYTSVTRHSRKF 60

QY 53 WCRGAIWRDCKILVKTSGSEQEVRDRVS IKDNQKRTFTVTMEDLMKTDADTYWCGIEK 112
DB 61 WCRBESGRCVTLASTGYTSQEYS-GRGKLTDFPDKGFVTVDTQNDSGSYKCGVGV 119

QY 113 TGN--DLGVTVQVTIDPAP---VTQETSSPTTLTGHHLDNRHKLKLSVLLPLFTI-- 165
DB 120 NGRGLDFGVNVLVSQKPEPDDVYKQYESYVTTITCPFYATRLQKK-----SFYKVED 173

QY 166 -XLLLVLAASLLAWRMKYQOKAAGMSPEQVLQPLEGLDLYADLTLOLAGTSPKATKL 224
DB 174 GELVLIIDSSKSEADPKYKGR-----ITLQIQSTAKEFTVTI 212

QY 225 SSAQVDQVEYVYTWMA---SLPKEDISYASLTGAEQDEPTYNMG 267
DB 213 KHLQNDAG-QYVCQSGSDPTAEQNVDLRLITPGL-----LYGNLG 253

RESULT 9
US-09-199-534-22
; Sequence 22, Application US/09199534
; Patent No. 6329569
; GENERAL INFORMATION:
; APPLICANT: Hein, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; TITLE OF INVENTION: SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 6329569th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199.534
; FILING DATE: 25-NOV-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/642,406
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/427,765
```

```
/
/ FILING DATE: 27-OCT-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Logan, April C.
/ REGISTRATION NUMBER: 33,950
/ REFERENCE/DOCKET NUMBER: 184.2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 554-2937
/ TELEFAX: (619) 554-6312
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 624 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-199-534-22

Query Match 10.6%; Score 159.5; DB 4; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLSGYSIAT-----QITGPTTVNGLERGLTVCQVYRSGMET--YLKW 52
Db 1 MALFLLTCLLAVFSAATAQSLLGPSSIFGPGEVNVLGDSVITCYPTTSTRSRKF 60
QY 53 WCRGAIWRDCKILVKISGSEQVYKDRVSIKDNQKNTFTVTMEDLMKTDADTYWCGIEK 112
Db 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPDKGEFVTVTDQNDSGSYKCGVGV 119
QY 113 TGN--DLGVTVQVITDPA---VTQETSSPTLTGHLDNRHKLKLSVLLPLIFTI-- 165
Db 120 NGRGLDFGVNVLVSQKPEPDVVYKQYESYVITTCPTVATRQLKK-----SFYKVED 173
QY 166 -XLLLLVAASLLAWRMKYQQAAGSPQVLPQLEGLDLCYADLTQLAGTSRKAATKL 224
Db 174 GELVLIIDSSSKAKDPYKGR-----ITLIQSTTAKEFTVTI 212
QY 225 SSAQVDQVEVEYVMA----SLPKEDISYASLTGLGAEDQPTVCNMG 267
Db 213 KHLQNDAG-QYVCQSGSDPTAEQVNDLRLTLPGL-----LYGNLG 253

RESULT 10
US-09-199-534-22
; Sequence 22, Application US/09199534
; Patent No. 6417429
; GENERAL INFORMATION:
; APPLICANT: Hein, Mich B.
; Hiatt, Andrew C.
; Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 6417429th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,534
; FILING DATE: 25-No. 6417429-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,406
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/427,765
```

```
/
/ FILING DATE: 27-OCT-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Logan, April C.
/ REGISTRATION NUMBER: 33,950
/ REFERENCE/DOCKET NUMBER: 184.2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 554-2937
/ TELEFAX: (619) 554-6312
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 624 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-199-534-22

Query Match 10.6%; Score 159.5; DB 4; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLSGYSIAT-----QITGPTTVNGLERGLTVCQVYRSGMET--YLKW 52
Db 1 MALFLLTCLLAVFSAATAQSLLGPSSIFGPGEVNVLGDSVITCYPTTSTRSRKF 60
QY 53 WCRGAIWRDCKILVKISGSEQVYKDRVSIKDNQKNTFTVTMEDLMKTDADTYWCGIEK 112
Db 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPDKGEFVTVTDQNDSGSYKCGVGV 119
QY 113 TGN--DLGVTVQVITDPA---VTQETSSPTLTGHLDNRHKLKLSVLLPLIFTI-- 165
Db 120 NGRGLDFGVNVLVSQKPEPDVVYKQYESYVITTCPTVATRQLKK-----SFYKVED 173
QY 166 -XLLLLVAASLLAWRMKYQQAAGSPQVLPQLEGLDLCYADLTQLAGTSRKAATKL 224
Db 174 GELVLIIDSSSKAKDPYKGR-----ITLIQSTTAKEFTVTI 212
QY 225 SSAQVDQVEVEYVMA----SLPKEDISYASLTGLGAEDQPTVCNMG 267
Db 213 KHLQNDAG-QYVCQSGSDPTAEQVNDLRLTLPGL-----LYGNLG 253

RESULT 11
US-08-434-000A-2
; Sequence 2, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; PRIOR APPLICATION DATA: 1
```


; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; TELETYPE: SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Mouse Polyimmunoglobulin Receptor
US-08-434-000A-8

Query Match 10.2%; Score 153; DB 3; Length 771;
Best Local Similarity 22.4%; Pred. No. 6.2e-07;
Matches 76; Conservative 46; Mismatches 144; Indels 74; Gaps 12;

QY 3 LTLTYLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYL-----KMWCRGA 57
DB 5 LFTLLVTVF--SGVSTKSPFPGQEVSSIEGDSVITCYYP---DTSVNRHTRKYWCRCQ 59
QY 58 IWRDCKILVTSQSEQVKRDRVSIKDNQKRTFTVIMEDLMKTDADTYWCGIEKTGNDL 117
DB 60 ASGMCCTLLISNGVLSKEYSGRANLINFENNTPVFNIEQLTQDDTGSYKCGLGTSNRGL 119
QY 118 GVTQVTTIDPAP-----VTQE-----ETSSPFTLTGHH 145
DB 120 SFDVLSVQVPELPSDTHVTVDIGRNVIECPFKRENVPKSKLCKTNQSCELV--- 176
QY 146 LDRHKKLLSVLLPLIF---TXLLLLVAASLLAWRMKYQQAAGMSPE-----Q 194
DB 177 IDSTEKVNPSYIGRAKLFPMKGTDLTVFYVNIHSLTHNDAGLYICQAGEGSPADKKMVDLQ 236
QY 195 VLQPLEGDLCYADLTQLA-----GTSPRKATTKLSSAQVDQVEVEYVTMAS----- 241
DB 237 VLAP--EPALLYKDLRSSVTFECDLGREVANEAKYLCRMNKETCDVIINTLGKRDPPDEGR 295

RESULT 14
US-09-312-157-8
; Sequence 8, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351
; SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Mouse Polyimmunoglobulin Receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-312-157-8

Query Match 10.2%; Score 153; DB 4; Length 771;
Best Local Similarity 22.4%; Pred. No. 6.2e-07;
Matches 76; Conservative 46; Mismatches 144; Indels 74; Gaps 12;

QY 3 LTLTYLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYL-----KMWCRGA 57
DB 5 LFTLLVTVF--SGVSTKSPFPGQEVSSIEGDSVITCYYP---DTSVNRHTRKYWCRCQ 59
QY 58 IWRDCKILVTSQSEQVKRDRVSIKDNQKRTFTVIMEDLMKTDADTYWCGIEKTGNDL 117
DB 60 ASGMCCTLLISNGVLSKEYSGRANLINFENNTPVFNIEQLTQDDTGSYKCGLGTSNRGL 119
QY 118 GVTQVTTIDPAP-----VTQE-----ETSSPFTLTGHH 145
DB 120 SFDVLSVQVPELPSDTHVTVDIGRNVIECPFKRENVPKSKLCKTNQSCELV--- 176
QY 146 LDRHKKLLSVLLPLIF---TXLLLLVAASLLAWRMKYQQAAGMSPE-----Q 194
DB 177 IDSTEKVNPSYIGRAKLFPMKGTDLTVFYVNIHSLTHNDAGLYICQAGEGSPADKKMVDLQ 236
QY 195 VLQPLEGDLCYADLTQLA-----GTSPRKATTKLSSAQVDQVEVEYVTMAS----- 241
DB 237 VLAP--EPALLYKDLRSSVTFECDLGREVANEAKYLCRMNKETCDVIINTLGKRDPPDEGR 295

RESULT 15
US-08-434-000A-10
; Sequence 10, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:31:24 ; Search time 117 Seconds
(without alignments)
782.054 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPLLTYLLFLWLSGYSIAT.....XSLPGRGPETPEYTSISR 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phage:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1493	99.6	290 4 Q7Z6A6	Q7Z6A6 homo sapien
2	1487	99.2	290 4 Q8TDQ1	Q8TDQ1 homo sapien
3	1408.5	94.0	293 4 Q7Z7I5	Q7Z7I5 homo sapien
4	803	53.6	244 4 Q8NAF5	Q8NAF5 homo sapien
5	727.5	48.5	165 4 Q7Z7I4	Q7Z7I4 homo sapien
6	725.5	48.4	194 4 Q8N6D0	Q8N6D0 homo sapien
7	550.5	36.7	283 11 Q8K4V9	Q8K4V9 mus musculus
8	451.5	30.1	201 4 Q8IX40	Q8IX40 homo sapien
9	451.5	30.1	238 4 Q8N6D1	Q8N6D1 homo sapien
10	367	24.5	314 11 Q7TSN3	Q7TSN3 mus musculus
11	367	24.5	318 11 Q7TN56	Q7TN56 mus musculus
12	364	24.3	318 11 Q8CFN3	Q8CFN3 mus musculus
13	358.5	23.9	221 11 Q8VCH2	Q8VCH2 mus musculus
14	351.5	23.4	221 11 Q8BRJ3	Q8BRJ3 mus musculus
15	331	22.1	299 4 Q9UBK4	Q9UBK4 homo sapien
16	330.5	22.0	298 4 Q9HD97	Q9HD97 homo sapien

17	330	22.0	299 4 Q9UGN4	Q9UGN4 homo sapien
18	323	21.5	301 4 Q9S100	Q9S100 homo sapien
19	263.5	17.6	196 11 Q8K249	Q8K249 mus musculus
20	254	16.9	205 4 Q7Z7I3	Q7Z7I3 homo sapien
21	247.5	16.5	223 11 Q8K4V8	Q8K4V8 mus musculus
22	238	15.9	230 11 Q7TSN2	Q7TSN2 mus musculus
23	235.5	15.7	228 11 Q7TN55	Q7TN55 mus musculus
24	231	15.4	228 11 Q8JZM5	Q8JZM5 mus musculus
25	230	15.3	287 11 Q9D7B8	Q9D7B8 mus musculus
26	230	15.3	332 4 Q8TA95	Q8TA95 homo sapien
27	227.5	15.2	222 4 Q8IX38	Q8IX38 homo sapien
28	227.5	15.2	233 4 Q8IX39	Q8IX39 homo sapien
29	227	15.1	257 11 Q8K4V7	Q8K4V7 mus musculus
30	155.5	10.4	209 11 Q9DAR9	Q9DAR9 mus musculus
31	154.5	10.3	206 11 Q8CHV3	Q8CHV3 mus musculus
32	151.5	10.1	186 4 Q9UMT0	Q9UMT0 homo sapien
33	150	10.0	733 6 Q8SQ83	Q8SQ83 trichosurus
34	143.5	9.6	311 4 Q8IYW2	Q8IYW2 homo sapien
35	143.5	9.6	313 4 Q86YW5	Q86YW5 homo sapien
36	142	9.5	532 4 Q8WVW6	Q8WVW6 homo sapien
37	142	9.5	534 4 Q96SA2	Q96SA2 homo sapien
38	142	9.5	731 6 Q8SPI6	Q8SPI6 macropus eu
39	140	9.3	758 6 Q9N2H7	Q9N2H7 sus scrofa
40	139.5	9.3	764 4 Q8IZY7	Q8IZY7 homo sapien
41	137.5	9.2	276 4 Q9H562	Q9H562 homo sapien
42	136.5	9.1	276 4 Q95944	Q95944 homo sapien
43	133.5	8.9	321 4 Q8IYW0	Q8IYW0 homo sapien
44	132	8.8	380 4 Q9H8E9	Q9H8E9 homo sapien
45	131.5	8.8	535 11 Q9EQ77	Q9EQ77 mus musculus

ALIGNMENTS

RESULT 1

Q7Z6A6	PRELIMINARY;	PRT;	290 AA.
AC Q7Z6A6;			
DT 01-OCT-2003 (TrEMBLrel. 25, Created)			
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE Inhibitory receptor IREM1.			
GN IREM1.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Alvarez-Erico D., Kitzig P., Sayos J., Lopez-Botet M.;			
RT "Molecular and functional characterization of IREM-1, a novel			
RT inhibitory receptor expressed by myeloid cells."			
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AY303545; AAP57942.1; "			
KW Receptor.			
SQ SEQUENCE 290 AA; 32354 MW; E9D84A6B417AA99B CRC64;			

Query Match	99.6%;	Score 1493;	DB 4;	Length 290;
Best Local Similarity	99.0%;	Pred. No. 9e-134;		
Matches 287;	Conservative	0; Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MPLLTYLLFLWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR	60	
Db	1	MPLLTYLLFLWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR	60	
Qy	61	DKILVKTSGSQEYKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEXTGNDLGV	120	
Db	61	DKILVKTSGSQEYKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEXTGNDLGV	120	
Qy	121	VQVTTDPAPVTOEETSSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM	180	
Db	121	VQVTTDPAPVTOEETSSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM	180	


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QY 181 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 240
DB 181 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 240

QY 241 SLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 290
DB 241 SLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 290

RESULT 2
Q8TD01 PRELIMINARY; PRT; 290 AA.
AC Q8TD01;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE NK inhibitory receptor.
GN NKIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Wan T., Zhang W., Cao X.;
RT "Novel human NK inhibitory receptor NKIR precursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251706; AAM19099.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001986; EFSF_synth.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00104; EFSF SYNTHASE_1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 290 AA; 32395 MW; D14FC04A047AAD10 CRC64;

Query Match 99.2%; Score 1487; DB 4; Length 290;
Best Local Similarity 98.6%; Pred. No. 3.e-133;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLS-GYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCRCGAIW 60
DB 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCRCGAIW 60

QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLVLLPLIFTIXLLLVAAALLAWR 180
DB 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLVLLPLIFTIXLLLVAAALLAWR 180

QY 181 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 240
DB 181 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 240

QY 241 SLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 290
DB 241 SLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 290

RESULT 3
Q7Z7I5 PRELIMINARY; PRT; 293 AA.
AC Q7Z7I5;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 1.
GN IREM1.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel
RT inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375480; AAP42152.1; -.
KW Receptor.
SQ SEQUENCE 293 AA; 32655 MW; 665BEA2F8D3CF43E CRC64;

Query Match 94.0%; Score 1408.5; DB 4; Length 293;
Best Local Similarity 94.5%; Pred. No. 1e-125;
Matches 275; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 MPELLTYLLFWLS-GYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCRCGAIW 59
DB 3 LPQLDMRVISAKSQYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCRCGAIW 62

QY 60 RCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
DB 63 RCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122

QY 120 TVQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLVLLPLIFTIXLLLVAAALLAWR 179
DB 123 TVQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLVLLPLIFTIXLLLVAAALLAWR 182

QY 180 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 239
DB 183 MKYQQAAGMSPEQVLQPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVYMA 242

QY 240 ASLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 290
DB 243 ASLPKEDISYASLTILGAEDQDEPTCYNMGLSSXLPGRGPEEPTSTISRP 293

RESULT 4
Q8NAF5 PRELIMINARY; PRT; 244 AA.
AC Q8NAF5;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ35438.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Small intestine;
RA Ninomiya K., Wagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saio K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092757; BAC03966.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 26643 MW; 2C7C6EAD5F9C7FA5 CRC64;

Query Match 53.6%; Score 803; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 3.8e-68;

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Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
Db 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
RESULT 5
Q72714 PRELIMINARY; PRT; 165 AA.
AC Q72714
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 2.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitsig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel
RT inhibitory receptor expressed by myeloid cells."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375481; AAP42153.1; -
KW Receptor.
SQ SEQUENCE 165 AA; 18655 MW; F163D7D366063099 CRC64;
Query Match 48.5%; Score 727.5; DB 4; Length 165;
Best Local Similarity 91.4%; Pred. No. 3.5e-61;
Matches 138; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
QY 1 MPLLTLVLLFWLS - GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 3 LPQLDLMRVISAQSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIW 62
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 63 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122
QY 120 TVQVITDPAVPTQETSSPILTGHHLDNR 148
Db 123 TVQVITDPAVPTQETSSPILTGHHLDNR 151
RESULT 6
Q72714 PRELIMINARY; PRT; 165 AA.
AC Q72714
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028199; AAH28199.1; -
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DR GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 194 AA; 21399 MW; 33B6AABE48F4FD6D CRC64;
Query Match 48.4%; Score 725.5; DB 4; Length 194;
Best Local Similarity 92.6%; Pred. No. 6.8e-61;
Matches 138; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 1 MPLLTLVLLFWLS - GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 3 LPQLDLMRVISAQSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIW 62
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 63 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122
QY 120 TVQVITDPAVPTQETSSPILTGHHLDNR 148
Db 123 TVQVITDPAVPTQETSSPILTGHHLDNR 151
RESULT 7
Q8K4V9 PRELIMINARY; PRT; 283 AA.
AC Q8K4V9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polymetric immunoglobulin receptor 3.
GN PIGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Li N., Chen T., Cao X.;
RT "Novel mouse PIGR3."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251703; AAM19096.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG-like.
DR SMART; SM00409; IG; 1.
KW Receptor.
SQ SEQUENCE 283 AA; 30777 MW; D6AC98F9C7FD5246 CRC64;
Query Match 36.7%; Score 550.5; DB 11; Length 283;
Best Local Similarity 40.2%; Pred. No. 5.3e-44;
Matches 132; Conservative 31; Mismatches 76; Indels 89; Gaps 6;
QY 1 MPLLTLVLLFWLSGYSIATQ - ITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 1 MHLSSLVPELFWITGCTAEDVPTGPEVSGQSGSVTVQCRYSQGWKDYKKYWCQGVQ 60
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 61 RSKTLIVETDASEQLVKNRVSIRDNQDFITVTMEDLRMSDAGIYWCITKGLDPMF 120
QY 120 TVQVITDPA - PVTQ - ETSSTSPILTGHHLDNRH - 150
Db 121 KVTNIGPAIQVPIVPTMPPITSTTTTFTVTTVKTSMEPTLTSYSDNGHGGSDSG 180
QY 151 - - - - - KLLKLSVLLPLIFTIXLLLVLAASLAWNMKYQQKAAGMSPEQVLPQLEGL 203
Db 181 GEDGVGDGFLDSVLLPVSIVALLHLIVA - - - - - 210
QY 204 CYADLTQLAGTSPRKATTKLSSAQVDQVEYVTMASLPKEDISYASLTGAEDQEPY 263
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Db 211 -----SSGKHQEEVYVYVMAFFPREEVSYAALTLAGLQGEPTY 249
QY 264 CNMGXLSXLPGRG-PPEPTREYSIRSP 290
Db 250 GNTGCPITHVPTGLGEEETYSIRSP 277

RESULT 8
Q8IX40
ID Q8IX40 PRELIMINARY; PRT; 201 AA.
AC Q8IX40.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TREM5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Colonna M.;
RT "Triggering receptor expressed on myeloid cells 5.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF427618; AAN86133.1; -.
DR InterPro; IPR003599; IG-like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 201 AA; 22689 MW; 258027A488B97CAF CRC64;

Query Match 30.1%; Score 451.5; DB 4; Length 201;
Best Local Similarity 49.8%; Pred. No. 9e-35; Indels 25; Gaps 8;
Matches 103; Conservative 22; Mismatches 57;

QY 8 LLLFWLSGYSIATQITGTTVNGLERGLTQCVYRSGWETYLKWCRCGAIWRCKILVK 67
Db 7 LLLLSLSG---CFSIQGPESVRAPEQSLTVQCHYKQGWETYLKWCRCGVRWDTCKILIE 63
QY 68 TSGSQEVRDRVSIKDNQKRTFTVTWEDLMKTDADTYWCGIEKTGNDLGVTVQVTDIP 127
Db 64 TRGSQGEKSDRVSIKDNQKRTFTVTWEGRLRRDADVIWCGIERRGPDJGTQVKVIVDP 123
QY 128 APVTQETSSSPT-----LTGHLDNRHKLKLSVLLPFTIXLLLVAAASLLAWRM 181
Db 124 EGAA-STTASPTNSNMAVFIGSHKRN-HYMLLVFKVPI-----LLILVTAIL--W--L 172
QY 182 KYQKAAGMSPEQVL-----QPLEGDL 203
Db 173 KGSQVRPPEPGEQPIYNNFSEPLTKDM 199

RESULT 9
Q8NGDI
ID Q8NGDI PRELIMINARY; PRT; 238 AA.
AC Q8NGDI;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor, CMRF35 antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT "Tissue-specific";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028091; AAH28091.1; -.
GO; GO:0004872; F:receptor activity; IEA.

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DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG_1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27020 MW; 1E7679BE434BB8B9 CRC64;

Query Match 30.1%; Score 451.5; DB 4; Length 238;
Best Local Similarity 49.8%; Pred. No. 1.1e-34; Indels 25; Gaps 8;
Matches 103; Conservative 22; Mismatches 57;

QY 8 LLLFWLSGYSIATQITGTTVNGLERGLTQCVYRSGWETYLKWCRCGAIWRCKILVK 67
Db 44 LLLLSLSG---CFSIQGPESVRAPEQSLTVQCHYKQGWETYLKWCRCGVRWDTCKILIE 100
QY 68 TSGSQEVRDRVSIKDNQKRTFTVTWEDLMKTDADTYWCGIEKTGNDLGVTVQVTDIP 127
Db 101 TRGSQGEKSDRVSIKDNQKRTFTVTWEGRLRRDADVIWCGIERRGPDJGTQVKVIVDP 160
QY 128 APVTQETSSSPT-----LTGHLDNRHKLKLSVLLPFTIXLLLVAAASLLAWRM 181
Db 161 EGAA-STTASPTNSNMAVFIGSHKRN-HYMLLVFKVPI-----LLILVTAIL--W--L 209
QY 182 KYQKAAGMSPEQVL-----QPLEGDL 203
Db 210 KGSQVRPPEPGEQPIYNNFSEPLTKDM 236

RESULT 10
Q7TSN3
ID Q7TSN3 PRELIMINARY; PRT; 314 AA.
AC Q7TSN3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MAIR-1a.
GN MAIR-1a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yotsumoto K., Okoshi Y., Shibuya K., Yamazaki S., Tahara-Hanaoka S.,
RA Honda S., Osawa M., Kuroiwa A., Matsuda Y., Tenen D.G., Iwana A.,
RA Nakauchi H., Shibuya A.;
RT "Paired Activating and Inhibitory Immunoglobulin-like Receptors, MAIR-1 and -1I, Regulate Mast Cell and Macrophage Activation.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091765; BAC77074.1; -.
SQ SEQUENCE 314 AA; 35259 MW; DEFF9509C3A1222D CRC64;

Query Match 24.5%; Score 367; DB 11; Length 314;
Best Local Similarity 34.5%; Pred. No. 1.9e-26; Indels 40; Gaps 13;
Matches 108; Conservative 52; Mismatches 113;

QY 1 MELLTLLYLLFWLSGYSIATQITGTTVNGLERGLTQCVYRSGWETYLKWCRCGAIWR 60
Db 10 LFTLLYLLFWLPG---CVPVHGSTMSGVSLSVSCRVEEFKTKDKTWCRVSLKI 66
QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTWEDLMKTDADTYWCGIE-----KTG 114
Db 67 LCKDIKTSSB-EARSGVTIRDPNLTFTVTVESLTLEDADTYMCAVDISLFDGSLG 125
QY 115 NDLGVTVQVTI---DPAPV--TQETSSPT-----LTGHLDNRHKLKLSVLLP 160
Db 126 FDYFKIELSVVPSDEPGTLETTPVYSTLPTKGPALGNTSGHREHYDSQGLRPLALLS 185
QY 161 LFTIXLLLVAAASLLAWRMKYQKAAGMSPE---QVLQPLEGDLCYADLTQLAGTSP 217
Db 186 -VLAULLFLVLTSLAWRMFKRLVKADRHPELSQNLRAQASEQNECOY-VNLQLHTWSL 243
QY 218 RKATTKLSSAQVDQVEVEVVTWASLPKEDISYASLTGAEDEPTYCNMGXLSXLPGRG 277

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Db 244 REEPVPSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD-SHANGDSLH-----QP 292
QY 278 PEEPTETSTSRP 290
Db 293 QDQKAEYSEIQKP 305

RESULT 11
ID Q7TNS6 PRELIMINARY; PRT; 318 AA.
AC Q7TNS6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mast cell-derived paired immunoglobulin-like receptor1.
GN MCFIR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/J;
RA MEDLINE=22774707; PubMed=12893283;
RA Kumagai H., Oki T., Tamitsu K., Feng S.-Z., Ono M., Nakajima H.,
RA Bao Y.-C., Kawakami Y., Nagayoshi K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Kawakami T., Kitamura T.
RT "Identification and characterization of a new pair of immunoglobulin-
RT like receptors LIM1 and 2 derived from murine bone marrow-derived
RT mast cells".
RL Biochem. Biophys. Res. Commun. 307:719-729(2003).
DR EMBL; AB095675; BAC80268.1; -.
KW Receptor.
SQ SEQUENCE 318 AA; 35654 MW; E5DA8BS6711EAS10 CRC64;

Query Match 24.5%; Score 367; DB 11; Length 318;
Best Local Similarity 34.4%; Pred. No. 1.9e-26;
Matches 109; Conservative 50; Mismatches 114; Indels 44; Gaps 12;

QY 1 MPELLTLLFLLFWSGYSIATQITGPTTVNGLERGLSTVQCVRSGWETYLKMWCRGAIWR 60
Db 10 LPTLLTLLFLLFPLPG---CVPLHGPTSMGSGVSGSLSVSCYEEKFKTKYWCGRSLKV 66
QY 61 DCKILVTSSEQEVKRDVSIKDNQKRTFTVMDLMTKTDADTYWCGIEKT--GNDLG 118
Db 67 LCKDIVTSSSE-EARSGRVTIRDPNLTFTVTYESLTLDADTYCAVDIPFFNAPLG 125
QY 119 VTQVTTIDPAPVTOETSSSPTLT-----GHLDNRHKL-----LKL 156
Db 126 LDKYFKIELSVVPSDDPVSSPGTLETPVVTSLPTKGPALGSNTEDRHDYSQGRLP 185
QY 157 VLLPLIFTIXLLLVAAASLLAWRMKYOQKAGKSPE---QVLPLEGDLCYADLTQLA 213
Db 186 ALLS-VLALLFLVGTSLTLLAWRMFKRLVKADRHPELSQNLQASEQNECQY-VNLQLH 243
QY 214 GTSPEKATTKLSAQQDQVEVEYVTVASLPKEDISYASLTLAGDDEPTCYNMGLSSXL 273
Db 244 TWSUREPVLPSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD-SHANGDSLH--- 294
QY 274 PGRGPEEPTETSTSRP 290
Db 295 --QPDQKAEYSEIQKP 309

RESULT 12
ID Q8CFN3 PRELIMINARY; PRT; 318 AA.
AC Q8CFN3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MMAC8 precursor (MAIR-IB).
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GN B230315M08RIK OR MMAC8 OR MAIR-IB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Yoshimoto M., Sekine S., Yazaki M., Sawada M.;
RT "Molecular cloning of an NK inhibitory receptor-related gene expressed
RT in a mouse microglial cell line, Ra2.".
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RA Yotsumoto K., Okoshi Y., Shibuya K., Yamazaki S., Tahara-Hanaka S.,
RA Honda S., Osawa M., Kuroiwa A., Matsuda Y., Tenen D.G., Iwama A.,
RA Nakauchi H., Shibuya A.;
RT "Paired Activating and Inhibitory Immunoglobulin-Like Receptors, MAIR-
RT I and -II, Regulate Mast Cell and Macrophage Activation.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB068156; BAC72S95.1; -.
DR EMBL; AB091766; BAC77075.1; -.
DR MGD; MGI:2443411; B230315M08RIK.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR01005; Myb_DNA_binding.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50838; IG_LIKE; 1.
DR PROSITE; PS00037; MYB_1; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 28 314 POTENTIAL.
SQ SEQUENCE 318 AA; 35629 MW; 490EDBD46AFA7C6 CRC64;

Query Match 24.3%; Score 364; DB 11; Length 318;
Best Local Similarity 34.1%; Pred. No. 3.6e-26;
Matches 108; Conservative 49; Mismatches 116; Indels 44; Gaps 11;

QY 1 MPELLTLLFLLFWSGYSIATQITGPTTVNGLERGLSTVQCVRSGWETYLKMWCRGAIWR 60
Db 10 LPTLLTLLFLLFPLPG---CVPLHGPTSMGSGVSGSLSVSCYEEKFKTKYWCVRSLKI 66
QY 61 DCKILVTSSEQEVKRDVSIKDNQKRTFTVMDLMTKTDADTYWCGIEKT--GNDLG 118
Db 67 LCKDIVTSSSE-EARSGRVTIRDPNLTFTVTYESLTLDADTYCAVDISLFDGSLG 125
QY 119 VTQVTTIDPAPVTOETSSSPTLT-----GHLDNRHKL-----LKL 156
Db 126 FKYFKIELSVVPSDDPVSSPGTLETPVVTSLPTKGPALGSNTEDRHDYSQGLRLP 185
QY 157 VLLPLIFTIXLLLVAAASLLAWRMKYOQKAGKSPE---QVLPLEGDLCYADLTQLA 213
Db 186 ALLS-VLALLFLVGTSLTLLAWRMFKRLVKADRHPELSQNLQASEQNECQY-VNLQLH 243
QY 214 GTSPEKATTKLSAQQDQVEVEYVTVASLPKEDISYASLTLAGDDEPTCYNMGLSSXL 273
Db 244 TWSUREPVLPSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD-SHANGDSLH--- 294
QY 274 PGRGPEEPTETSTSRP 290
Db 295 --QPDQKAEYSEIQKP 309

RESULT 13
ID Q8VCH2 PRELIMINARY; PRT; 221 AA.
AC Q8VCH2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
```

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GN 4732429D16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019814; AALH9814.1; -.
DR MGD; MGI:2442358; 4732429D16RIK.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 221 AA; 24954 MW; C9E6203BE64922C1 CRC64;

Query Match 23.9%; Score 358.5; DB 11; Length 221;
Best Local Similarity 44.3%; Pred. No. 7.4e-26;
Matches 85; Conservative 21; Mismatches 65; Indels 21; Gaps 3;

QY 8 LLLFWLGSYSIA-TQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWRDCKILV 66
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LLLFFLPGCCTAQSIVTGFEEVSGQSLTVQCRYSYWKYKGYKWCRCGVPQRSCLIV 66
QY 67 KTSGEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVTID 126
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 ETDKSEQLVKKNRVSIRDQDFITVTMEDLRMSDAGIYWCGITKGGPDPMFKNVNI 126
QY 127 PAPVTOEETSSPTL-----TGHLDNRHK-----LLKLSVLLPLIFTIX 166
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 QAPKSSMMTTTATVLKSIQPSAENTGKEQVTSKQEVTSRPHRTSLSSIVFLIMVFEL 186
QY 167 LLLLVAASLLAW 178
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
187 PLLLSMLSAVLW 198

RESULT 15
QUBK4 PRELIMINARY; PRT; 299 AA.
AC QUBK4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE IRL1 (Leukocyte membrane antigen).
GN IRL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA O'Connor C.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Antoni C.; Biassoni R.;
RT "Molecular cloning of a novel inhibitory receptor.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Antoni C.; Biassoni R.;
RT "IRL1 isoforms.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224864; CAB55347.1; -.
DR EMBL; AJ010101; CAB52291.1; -.
DR EMBL; BC032352; AHA32352.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 299 AA; 33201 MW; 978461DA87E86269 CRC64;

Query Match 22.1%; Score 331; DB 4; Length 299;
Best Local Similarity 33.2%; Pred. No. 4.7e-23;
Matches 105; Conservative 52; Mismatches 101; Indels 58; Gaps 14;

QY 8 LLLFWLGSYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWRDCKILV 67
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LLLLMVFEV---CFALSKCRFTVAGVGGSLVQCPKEHRTLNKYWRPPQIFLDCXIVE 63

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Qy 68 TSGSEQVKRDRVSIKDNQNRFTVTMEDLMKTDADTYWCGIE-----KTGNDLGVTYQV 123
Db 64 TXGSAGK-RNGRVSIKDRVSIKDNQNRFTVTMEDLMKTDADTYWCGIE-----KTGNDLGVTYQV 122
Qy 124 TI-----DPAPVTOETS-----SSPTL-----TGHHLNRRHL-----LKLSVL 158
Db 123 SVFPASTMTPASITAAKTITITAFPPVSTTLFAVGATHSASIQEETEVEVNSQLPLL 182
Qy 159 LPLIFTIXLLLVAAASLLAWRMKYQOKAA-----GMSPEQVLOPLEGDLCYADLTQLA 213
Db 183 LSLI-ALLLLLVGASLLAWRMFYQOKIKAGDHSELSONPKQA--ATQSELHYANLELLMW 239
Qy 214 GTSRKAATKLSAQVQVEVEVVTMASLPKEDISVASLTJGAEDQEPYCNNGXLSXL 273
Db 240 PLOEKAPPR-----EVEVEISTVAS-PRLEHVASVVFDS-----NTNRIAAQR 283
Qy 274 PGRGPEEFTYSTISR 289
Db 284 P-REEPDSYSVIRK 298

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Search completed: September 16, 2004, 12:39:49
Job time : 119 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:41:16 ; Search time 122 Seconds
(without alignments)
671.629 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290
Sequence: 1 MPLLTYLLFLWLSGVSIAT.....SXLPGRPPEPTFEYTIISRP 290

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	287	99.0	291	3	AAB32379 Human sec
2	166	57.2	290	4	AAB74712 Human mem
3	166	57.2	290	5	AAB83611 Human PRO
4	166	57.2	290	6	ABU80758 Human PRO
5	166	57.2	290	6	ABO33724 Novel hum
6	166	57.2	290	6	ABU82067 Novel hum
7	166	57.2	290	6	ABJ72247 Human PRO
8	166	57.2	290	6	ABJ72375 Human PRO
9	166	57.2	290	6	ABO34270 Human sec
10	166	57.2	290	7	ABJ72077 Human mem
11	166	57.2	290	7	ADB83530 Novel hum
12	166	57.2	290	7	ADB80636 Novel hum
13	166	57.2	290	7	ADB73177 Novel hum
14	166	57.2	290	7	ADB78259 Novel hum
15	166	57.2	290	7	ADB84907 Human PRO
16	166	57.2	290	7	ADB78013 Novel hum
17	166	57.2	290	7	ADB87079 Human PRO
18	166	57.2	290	7	ADB84661 Human PRO
19	166	57.2	290	7	ADB83776 Novel hum
20	166	57.2	290	7	ADB72931 Novel hum
21	166	57.2	290	7	ADC36769 Human PRO
22	166	57.2	290	7	ADC21759 Human PRO
23	166	57.2	290	7	ADC49790 Novel hum
24	166	57.2	290	7	ADC48989 Novel hum
25	166	57.2	290	7	ADC49506 Novel hum

99	10	3.4	201	6	ABU88251	Novel	hum	172	10	3.4	201	6	ABU86186	Novel	hum
100	10	3.4	201	6	ABU84566	Human	sec	173	10	3.4	201	6	ABU82473	Novel	hum
101	10	3.4	201	6	ABR66440	Human	sec	174	10	3.4	201	6	ABU87484	Human	PRO
102	10	3.4	201	6	ABR65830	Human	sec	175	10	3.4	201	6	ABU83956	Human	sec
103	10	3.4	201	6	ABR65830	Human	sec	176	10	3.4	201	6	ABO08330	Human	PRO
104	10	3.4	201	6	ABU99770	Human	sec	177	10	3.4	201	6	ABO08330	Human	PRO
105	10	3.4	201	6	ABU83009	Human	PRO	178	10	3.4	201	6	ABU82041	Novel	hum
106	10	3.4	201	6	ABU90130	Novel	hum	179	10	3.4	201	6	ABU66205	Novel	hum
107	10	3.4	201	6	ABR68379	Human	sec	180	10	3.4	201	6	ABU60034	Human	sec
108	10	3.4	201	6	ABU96432	Novel	hum	181	10	3.4	201	6	ABU94222	Novel	hum
109	10	3.4	201	6	ABU92863	Human	sec	182	10	3.4	201	6	ABO00095	Novel	hum
110	10	3.4	201	6	ABO08940	Human	sec	183	10	3.4	201	6	ABR66745	Human	sec
111	10	3.4	201	6	ABO02992	Human	sec	184	10	3.4	201	6	ABR91163	Human	sec
112	10	3.4	201	6	ABR75146	Human	sec	185	10	3.4	201	6	ABR94590	Human	PRO
113	10	3.4	201	6	ABR94908	Human	sec	186	10	3.4	201	6	ABU79472	Human	PRO
114	10	3.4	201	6	ABU85881	Human	PRO	187	10	3.4	201	6	ABU86801	Human	sec
115	10	3.4	201	6	ABU99041	Novel	hum	188	10	3.4	201	6	ABU87106	Novel	hum
116	10	3.4	201	6	ABU98256	Novel	hum	189	10	3.4	201	6	ABU94895	Human	PRO
117	10	3.4	201	6	ABU91962	Novel	hum	190	10	3.4	201	6	ABO04822	Human	PRO
118	10	3.4	201	6	ABU83655	Human	PRO	191	10	3.4	201	6	ABR70571	Human	sec
119	10	3.4	201	6	ABU86496	Human	sec	192	10	3.4	201	6	ABU98736	Human	PRO
120	10	3.4	201	6	ABU67709	Human	sec	193	10	3.4	201	6	ABR66135	Human	sec
121	10	3.4	201	6	ABU80737	Human	PRO	194	10	3.4	201	6	ABU79777	Human	PRO
122	10	3.4	201	6	ABR99655	Human	sec	195	10	3.4	201	6	ABU93168	Human	sec
123	10	3.4	201	6	ABR99045	Human	sec	196	10	3.4	201	6	ABU96127	Human	PRO
124	10	3.4	201	6	ABO14568	Human	sec	197	10	3.4	201	6	ABU91347	Novel	hum
125	10	3.4	201	6	ABR92468	Human	sec	198	10	3.4	201	6	ABU90440	Novel	hum
126	10	3.4	201	6	ABO19109	Human	sec	199	10	3.4	201	6	ABO09855	Human	sec
127	10	3.4	201	6	ABR78530	Human	sec	200	10	3.4	201	6	ABO11127	Human	sec
128	10	3.4	201	6	ABU85266	Novel	hum	201	10	3.4	201	6	ABR71181	Human	sec
129	10	3.4	201	6	ABO00405	Novel	hum	202	10	3.4	201	6	ABU87789	Human	PRO
130	10	3.4	201	6	ABO11737	Human	sec	203	10	3.4	201	6	ABU91657	Human	PRO
131	10	3.4	201	6	ABO02382	Human	sec	204	10	3.4	201	6	ABU84871	Human	sec
132	10	3.4	201	6	ABU88956	Novel	hum	205	10	3.4	201	6	ABR69561	Human	sec
133	10	3.4	201	6	ABU83651	Human	sec	206	10	3.4	201	6	ABU80338	Human	PRO
134	10	3.4	201	6	ABO06452	Novel	hum	207	10	3.4	201	6	ABU93607	Human	PRO
135	10	3.4	201	6	ABR59488	Human	sec	208	10	3.4	201	6	ABO10160	Human	sec
136	10	3.4	201	6	ABO09550	Human	sec	209	10	3.4	201	6	ABO09245	Human	sec
137	10	3.4	201	6	ABO119414	Novel	hum	210	10	3.4	201	6	ABU10813	Human	sec
138	10	3.4	201	6	ABO11432	Human	sec	211	10	3.4	201	6	ABU95822	Human	PRO
139	10	3.4	201	6	ABR67050	Human	sec	212	10	3.4	201	6	ABU97031	Novel	hum
140	10	3.4	201	6	ABO16263	Human	sec	213	10	3.4	201	6	ABU70876	Human	sec
141	10	3.4	201	6	ABO13969	Human	sec	214	10	3.4	201	6	ABO05227	Novel	hum
142	10	3.4	201	6	ABU65872	Human	sec	215	10	3.4	201	6	ABO08635	Human	sec
143	10	3.4	201	6	ABO07720	Human	PRO	216	10	3.4	201	6	ABO05842	Human	sec
144	10	3.4	201	6	ABO03907	Human	sec	217	10	3.4	201	6	ABR74231	Human	sec
145	10	3.4	201	6	ABR67355	Human	sec	218	10	3.4	201	6	ABR95823	Human	sec
146	10	3.4	201	6	ABO15958	Human	sec	219	10	3.4	201	6	ABR81120	Human	sec
147	10	3.4	201	6	ABU56239	Human	sec	220	10	3.4	201	6	ABR81120	Human	sec
148	10	3.4	201	6	ABU65567	Human	PRO	221	10	3.4	201	6	ABR81121	Human	sec
149	10	3.4	201	6	ABU95512	Novel	hum	222	10	3.4	201	6	ABR88723	Human	sec
150	10	3.4	201	6	ABU71415	Human	PRO	223	10	3.4	201	6	ABR77544	Human	sec
151	10	3.4	201	6	ABO08025	Human	PRO	224	10	3.4	201	6	ABR77544	Human	sec
152	10	3.4	201	6	ABR70266	Human	sec	225	10	3.4	201	6	ABO29028	Human	sec
153	10	3.4	201	6	ABR69599	Human	sec	226	10	3.4	201	6	ABO31773	Human	sec
154	10	3.4	201	6	ABU81542	Human	PRO	227	10	3.4	201	6	ABO08190	Human	sec
155	10	3.4	201	6	ABR60339	Human	sec	228	10	3.4	201	6	ABO40670	Human	sec
156	10	3.4	201	6	ABR68074	Human	sec	229	10	3.4	201	6	ABO40670	Human	sec
157	10	3.4	201	6	ABR65462	Human	sec	230	10	3.4	201	6	ABO44234	Human	PRO
158	10	3.4	201	6	ABR68684	Human	sec	231	10	3.4	201	6	ABO44234	Human	sec
159	10	3.4	201	6	ABR72096	Human	sec	232	10	3.4	201	6	ABO36095	Human	PRO
160	10	3.4	201	6	ABU85576	Human	PRO	233	10	3.4	201	6	ABO36095	Human	PRO
161	10	3.4	201	6	ABU83346	Human	sec	234	10	3.4	201	6	ABO44234	Human	sec
162	10	3.4	201	6	ABU83346	Human	sec	235	10	3.4	201	6	ADA78360	Human	sec
163	10	3.4	201	6	ABU95202	Novel	hum	236	10	3.4	201	6	ABM25029	Human	sec
164	10	3.4	201	6	ABU90750	Novel	hum	237	10	3.4	201	6	ABO21756	Human	sec
165	10	3.4	201	6	ABU84261	Human	sec	238	10	3.4	201	6	ABR98020	Human	sec
166	10	3.4	201	6	ABU93912	Novel	hum	239	10	3.4	201	6	ABR87808	Human	sec
167	10	3.4	201	6	ABR65157	Human	sec	240	10	3.4	201	6	ABM77849	Human	sec
168	10	3.4	201	6	ABR68989	Human	sec	241	10	3.4	201	6	ABM77849	Human	sec
169	10	3.4	201	6	ABO06805	Human	sec	242	10	3.4	201	6	ABM28079	Human	sec
170	10	3.4	201	6	ABR99350	Human	sec	243	10	3.4	201	6	ABM06360	Human	sec
171	10	3.4	201	6	ABU57234	Human	PRO	244	10	3.4	201	6	ABM03866	Human	sec
													ABM35317	Human	sec

245	10	3.4	201	6	ABM26554	Abm26554 Human sec	318	10	3.4	201	6	ABM75105	Abm75105 Human sec
246	10	3.4	201	6	ABO48336	AbO48336 Human sec	319	10	3.4	201	6	ADA80152	Ada80152 Human sec
247	10	3.4	201	6	ABR93078	AbR93078 Human sec	320	10	3.4	201	6	ABR96495	AbR96495 Human sec
248	10	3.4	201	6	ABO24839	AbO24839 Human sec	321	10	3.4	201	6	ABM02646	Abm02646 Human sec
249	10	3.4	201	6	ABM11850	Abm11850 Human sec	322	10	3.4	201	6	ABR86588	AbR86588 Human sec
250	10	3.4	201	6	ABM02951	Abm02951 Human sec	323	10	3.4	201	6	ABR86893	AbR86893 Human sec
251	10	3.4	201	6	ABM16247	Abm16247 Human sec	324	10	3.4	201	6	ABM16857	Abm16857 Human sec
252	10	3.4	201	6	ABO27808	AbO27808 Human sec	325	10	3.4	201	6	ABM29909	Abm29909 Human sec
253	10	3.4	201	6	ABM92929	Abm92929 Human sec	326	10	3.4	201	6	ABO29333	AbO29333 Human sec
254	10	3.4	201	6	ABM07275	Abm07275 Human sec	327	10	3.4	201	6	ABM24114	Abm24114 Human sec
255	10	3.4	201	6	ABM21369	Abm21369 Human sec	328	10	3.4	201	6	ABM23504	Abm23504 Human sec
256	10	3.4	201	6	ABM09715	Abm09715 Human sec	329	10	3.4	201	6	ABM22284	Abm22284 Human sec
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258	10	3.4	201	6	ABO36400	AbO36400 Human PRO	331	10	3.4	201	6	ABM28689	Abm28689 Human sec
259	10	3.4	201	6	ABO43929	AbO43929 Human PRO	332	10	3.4	201	6	ABM28994	Abm28994 Human sec
260	10	3.4	201	6	ABM76629	Abm76629 Human sec	333	10	3.4	201	6	ABM66638	Abm66638 Human sec
261	10	3.4	201	6	ABM76325	Abm76325 Human sec	334	10	3.4	201	6	ABM76020	Abm76020 Human sec
262	10	3.4	201	6	ABM25944	Abm25944 Human sec	335	10	3.4	201	6	ABM34300	Abm34300 Human sec
263	10	3.4	201	6	ABM96249	Abm96249 Human sec	336	10	3.4	201	6	ABM34605	Abm34605 Human sec
264	10	3.4	201	6	ABO3602	AbO3602 Human sec	337	10	3.4	201	6	ABO20536	AbO20536 Human sec
265	10	3.4	201	6	ABO2687	AbO2687 Human sec	338	10	3.4	201	6	ABO21451	AbO21451 Human sec
266	10	3.4	201	6	ABR90858	AbR90858 Human sec	339	10	3.4	201	6	ABO22366	AbO22366 Human sec
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268	10	3.4	201	6	ABO17178	AbO17178 Human sec	341	10	3.4	201	6	ABR85978	AbR85978 Human sec
269	10	3.4	201	6	ABR94603	AbR94603 Human sec	342	10	3.4	201	6	ABR99960	AbR99960 Human sec
270	10	3.4	201	6	ABR76110	AbR76110 Human sec	343	10	3.4	201	6	ABM00511	Abm00511 Human sec
271	10	3.4	201	6	ABR71486	AbR71486 Human sec	344	10	3.4	201	6	ABM00816	Abm00816 Human sec
272	10	3.4	201	6	ABR93383	AbR93383 Human sec	345	10	3.4	201	6	ABO29943	AbO29943 Human sec
273	10	3.4	201	6	ABR93688	AbR93688 Human sec	346	10	3.4	201	6	ABM23809	Abm23809 Human sec
274	10	3.4	201	6	ABR88113	AbR88113 Human sec	347	10	3.4	201	6	ABM29604	Abm29604 Human sec
275	10	3.4	201	6	ABO28113	AbO28113 Human sec	348	10	3.4	201	6	ABO38535	AbO38535 Human sec
276	10	3.4	201	6	ABO30248	AbO30248 Human sec	349	10	3.4	201	6	ABO45835	AbO45835 Human PRO
277	10	3.4	201	6	ABO33457	AbO33457 Human PRO	350	10	3.4	201	6	ABM20759	Abm20759 Human sec
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279	10	3.4	201	6	ABM09105	Abm09105 Human sec	352	10	3.4	201	6	ABO16873	AbO16873 Human sec
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282	10	3.4	201	6	ABO39755	AbO39755 Human sec	355	10	3.4	201	6	ABO23231	AbO23231 Human PRO
283	10	3.4	201	6	ABM10630	Abm10630 Human sec	356	10	3.4	201	6	ABR92773	AbR92773 Human sec
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286	10	3.4	201	6	ABO52606	AbO52606 Human PRO	359	10	3.4	201	6	ABR89943	AbR89943 Human sec
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291	10	3.4	201	6	ABM48384	Abm48384 Human sec	364	10	3.4	201	6	ABM07580	Abm07580 Human sec
292	10	3.4	201	6	ABO32383	AbO32383 Human sec	365	10	3.4	201	6	ABM04171	Abm04171 Human sec
293	10	3.4	201	6	ABM15510	Abm15510 Human sec	366	10	3.4	201	6	ABO37315	AbO37315 Human sec
294	10	3.4	201	6	ABM06665	Abm06665 Human sec	367	10	3.4	201	6	ABO41890	AbO41890 Human sec
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296	10	3.4	201	6	ABM22589	Abm22589 Human sec	369	10	3.4	201	6	ABM25334	Abm25334 Human sec
297	10	3.4	201	6	ABM07885	Abm07885 Human sec	370	10	3.4	201	6	ABO47726	AbO47726 Human sec
298	10	3.4	201	6	ABO40975	AbO40975 Human sec	371	10	3.4	201	6	ABO48031	AbO48031 Human sec
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300	10	3.4	201	6	ABM33385	Abm33385 Human sec	373	10	3.4	201	6	ABO51691	AbO51691 Human PRO
301	10	3.4	201	6	ABO52911	AbO52911 Human PRO	374	10	3.4	201	6	ABO51996	AbO51996 Human PRO
302	10	3.4	201	6	ABO50471	AbO50471 Human sec	375	10	3.4	201	6	ABO50776	AbO50776 Human sec
303	10	3.4	201	6	ABU99465	Abu99465 Human sec	376	10	3.4	201	6	ABR79900	AbR79900 Human sec
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305	10	3.4	201	6	ABR18687	AbR18687 Human sec	378	10	3.4	201	6	ABO18194	AbO18194 Human sec
306	10	3.4	201	6	ABR97715	AbR97715 Human sec	379	10	3.4	201	6	ABO21146	AbO21146 Human sec
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309	10	3.4	201	6	ABR89028	AbR89028 Human sec	382	10	3.4	201	6	ABM16552	Abm16552 Human sec
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311	10	3.4	201	6	ABM21064	Abm21064 Human sec	384	10	3.4	201	6	ABM14900	Abm14900 Human sec
312	10	3.4	201	6	ABO42195	AbO42195 Human sec	385	10	3.4	201	6	ABM04781	Abm04781 Human sec
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315	10	3.4	201	6	ABO38840	AbO38840 Human sec	388	10	3.4	201	6	ABO39450	AbO39450 Human sec
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317	10	3.4	201	6	ABM22894	Abm22894 Human sec	390	10	3.4	201	6	ABM25639	Abm25639 Human sec

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392	10	3.4	201	6	ABO47055	Human PRO	465	10	3.4	201	7	ABO29638	Human sec
393	10	3.4	201	6	ABO47360	Human PRO	466	10	3.4	201	7	ABO31468	Human sec
394	10	3.4	201	6	ADA83677	Human sec	467	10	3.4	201	7	ABM14595	Human sec
395	10	3.4	201	6	ABR71791	Human sec	468	10	3.4	201	7	ABM10020	Human sec
396	10	3.4	201	6	ABR72401	Human sec	469	10	3.4	201	7	ABO39145	Human sec
397	10	3.4	201	6	ABR98740	Human sec	470	10	3.4	201	7	ABM34910	Human sec
398	10	3.4	201	6	ABO07110	Human sec	471	10	3.4	201	7	ABO51386	Human sec
399	10	3.4	201	6	ABR85063	Human sec	472	10	3.4	201	7	ABO04212	Human sec
400	10	3.4	201	6	ABR73621	Human sec	473	10	3.4	201	7	ABO10682	Human PRO
401	10	3.4	201	6	ABR76715	Human sec	474	10	3.4	201	7	ABR77925	Human sec
402	10	3.4	201	6	ABR73316	Human sec	475	10	3.4	201	7	ABR79135	Human sec
403	10	3.4	201	6	ABM18382	Human sec	476	10	3.4	201	7	ABO24229	Human sec
404	10	3.4	201	6	ABO20841	Human sec	477	10	3.4	201	7	ABR93993	Human sec
405	10	3.4	201	6	ABO25584	Human PRO	478	10	3.4	201	7	ABM02036	Human sec
406	10	3.4	201	6	ABO25889	Human PRO	479	10	3.4	201	7	ABM78459	Human sec
407	10	3.4	201	6	ABR94298	Human sec	480	10	3.4	201	7	ABR90248	Human sec
408	10	3.4	201	6	ABR80205	Human sec	481	10	3.4	201	7	ABM27774	Human sec
409	10	3.4	201	6	ABM11545	Human sec	482	10	3.4	201	7	ABM13375	Human sec
410	10	3.4	201	6	ABO33152	Human PRO	483	10	3.4	201	7	ABO32078	Human sec
411	10	3.4	201	6	ABO30858	Human sec	484	10	3.4	201	7	ABM14290	Human sec
412	10	3.4	201	6	ABO331163	Human sec	485	10	3.4	201	7	ABM08495	Human sec
413	10	3.4	201	6	ABM27469	Human sec	486	10	3.4	201	7	ABO40365	Human sec
414	10	3.4	201	6	ABM30214	Human sec	487	10	3.4	201	7	ABM74800	Human sec
415	10	3.4	201	6	ABM05750	Human sec	488	10	3.4	201	7	ABM33395	Human sec
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418	10	3.4	201	6	ABO42500	Human sec	491	10	3.4	201	7	ABR73011	Human sec
419	10	3.4	201	6	ABO38230	Human sec	492	10	3.4	201	7	ABO15653	Human sec
420	10	3.4	201	6	ABO46140	Human PRO	493	10	3.4	201	7	ABR85368	Human sec
421	10	3.4	201	6	ABM66943	Human sec	494	10	3.4	201	7	ABO15348	Human sec
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423	10	3.4	201	6	ABM19844	Human sec	496	10	3.4	201	7	ABM17772	Human sec
424	10	3.4	201	6	ABO49556	Human sec	497	10	3.4	201	7	ABR85673	Human sec
425	10	3.4	201	6	ABO49861	Human sec	498	10	3.4	201	7	ABM77239	Human sec
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427	10	3.4	201	6	ABR88418	Human sec	500	10	3.4	201	7	ABM23199	Human sec
428	10	3.4	201	6	ABM27164	Human sec	501	10	3.4	201	7	ABM30519	Human sec
429	10	3.4	201	6	ABM03561	Human sec	502	10	3.4	201	7	ABM21579	Human sec
430	10	3.4	201	7	ABO40060	Human sec	503	10	3.4	201	7	ABM21674	Human sec
431	10	3.4	201	7	ABO50166	Human sec	504	10	3.4	201	7	ABM15205	Human sec
432	10	3.4	201	7	ABO51081	Human sec	505	10	3.4	201	7	ABO41280	Human sec
433	10	3.4	201	7	ABO05537	Human sec	506	10	3.4	201	7	ABO37010	Human sec
434	10	3.4	201	7	ABR74841	Human sec	507	10	3.4	201	7	ABO37620	Human sec
435	10	3.4	201	7	ABR77320	Human sec	508	10	3.4	201	7	ABM75410	Human sec
436	10	3.4	201	7	ABM18077	Human sec	509	10	3.4	201	7	ABM33690	Human sec
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438	10	3.4	201	7	ABO22061	Human sec	511	10	3.4	201	7	ADA83043	Human sec
439	10	3.4	201	7	ABO20231	Human sec	512	10	3.4	201	7	ABM32044	Human sec
440	10	3.4	201	7	ABO24534	Human sec	513	10	3.4	201	7	ABM31434	Human sec
441	10	3.4	201	7	ABR86283	Human sec	514	10	3.4	201	7	ABR86351	Human sec
442	10	3.4	201	7	ABM10935	Human sec	515	10	3.4	201	7	ABM32349	Human sec
443	10	3.4	201	7	ABM16934	Human sec	516	10	3.4	201	7	ABM32854	Human sec
444	10	3.4	201	7	ABR89638	Human sec	517	10	3.4	201	7	ABM31739	Human sec
445	10	3.4	201	7	ABM12765	Human sec	518	10	3.4	201	7	ABM31129	Human sec
446	10	3.4	201	7	ABM06055	Human sec	519	10	3.4	201	7	ADD06081	Human sec
447	10	3.4	201	7	ABO35180	Human PRO	520	10	3.4	201	7	ADD10633	Human sec
448	10	3.4	201	7	ABM03256	Human sec	521	10	3.4	201	7	ADD11593	Human sec
449	10	3.4	201	7	ABM19234	Human sec	522	10	3.4	201	7	ADD37386	Human sec
450	10	3.4	201	7	ABM19539	Human sec	523	10	3.4	201	8	AD541594	Human sec
451	10	3.4	201	7	ABO46750	Human PRO	524	10	3.4	201	8	AD541594	Human sec
452	10	3.4	201	7	ABO49251	Human sec	525	10	3.4	201	8	AD574745	Human sec
453	10	3.4	201	7	ABR69294	Human sec	526	10	3.4	201	8	AD575357	Human sec
454	10	3.4	201	7	ABR89323	Human sec	527	9	3.1	194	5	ABR80581	Human TRB
455	10	3.4	201	7	ABR72706	Human sec	528	9	3.1	619	7	ABR80581	Human sbg
456	10	3.4	201	7	ABR74536	Human sec	529	9	3.1	619	7	AD568456	S. arundi
457	10	3.4	201	7	ABO18804	Human sec	530	9	3.1	623	7	AD568456	S. arundi
458	10	3.4	201	7	ABR80510	Human sec	531	9	3.1	1102	6	ABU39716	Protein e
459	10	3.4	201	7	ABM01731	Human sec	532	8	2.8	37	2	Ay11486	Human 5'
460	10	3.4	201	7	ABM02341	Human sec	533	8	2.8	48	3	AAy94979	Human pro
461	10	3.4	201	7	ABR87503	Human sec	534	8	2.8	48	3	AAy94872	Human pro
462	10	3.4	201	7	ABM13070	Human sec	535	8	2.8	48	7	AD511769	Human sec
463	10	3.4	201	7	ABM30824	Human sec	536	8	2.8	49	3	AAy76146	Human sec

537	8	2.8	64	6	ADA56926	Ada56926 Human sec	610	7	2.4	107	3	AAB15813	Aab15813 Human che
538	8	2.8	64	6	ADA40776	Ada40776 Human sec	611	7	2.4	107	5	ABP65256	Abp65256 Hypoxia-r
539	8	2.8	65	6	AAAY07904	Aay07904 Human sec	612	7	2.4	107	6	ABU57617	Abu57617 Different
540	8	2.8	83	6	ABJ37115	Abj37115 NOVX prot	613	7	2.4	107	6	ABU57618	Abu57618 Different
541	8	2.8	90	6	ABJ37116	Abj37116 NOVX prot	614	7	2.4	107	6	ABU67715	Abu67715 Human CX
542	8	2.8	102	6	AAAR70793	Aar70793 Gro-Beta/	615	7	2.4	107	7	ABO07349	Abo07349 Amino aci
543	8	2.8	103	6	ABJ37114	Abj37114 NOVX prot	616	7	2.4	107	7	ADC78819	Adc78819 Human PRO
544	8	2.8	103	6	ABJ37113	Abj37113 NOVX prot	617	7	2.4	107	7	ABO07349	Abo07349 Human PRO
545	8	2.8	107	2	AAAR20304	Aar20304 Human GRO	618	7	2.4	109	4	AAO10848	Aao10848 Human ORF
546	8	2.8	107	2	AAAR20589	Aar20589 Human mac	619	7	2.4	109	5	ABP33528	Abp33528 Human ORF
547	8	2.8	107	2	AAAR20529	Aar20529 Human mac	620	7	2.4	115	2	AAU12637	Aau12637 Human 5'
548	8	2.8	107	2	AAAR20590	Aar20590 Human mac	621	7	2.4	119	4	AAU32860	Aau32860 Novel hum
549	8	2.8	107	2	AAAR20530	Aar20530 Human mac	622	7	2.4	120	4	AAW07542	Aaw07542 Clone 99,
550	8	2.8	107	2	AAAR70794	Aar70794 Gro-Gamma	623	7	2.4	120	7	ABO23587	Abo23587 Neisseria
551	8	2.8	107	2	AAW96714	Aaw96714 Growth re	624	7	2.4	124	3	AAU64704	Aau64704 Human 5'
552	8	2.8	107	2	ABAB15810	Abab15810 Human che	625	7	2.4	134	3	AAU43145	Aau43145 Arabidops
553	8	2.8	107	5	ABP65254	Abp65254 Hypoxia-r	626	7	2.4	134	3	AAU15572	Aau15572 Arabidops
554	8	2.8	107	6	ABU67715	Abu67715 Human COP	627	7	2.4	136	4	AAU07337	Aau07337 1-aminocy
555	8	2.8	107	6	ABU67716	Abu67716 Human CX	628	7	2.4	143	3	AAU15571	Aau15571 Arabidops
556	8	2.8	107	6	ABU67716	Abu67716 Human CX	629	7	2.4	143	3	AAU15571	Aau15571 Arabidops
557	8	2.8	107	7	ABO07350	Abo07350 Amino aci	630	7	2.4	143	5	ABG71687	Abg71687 Human mac
558	8	2.8	125	5	ABP31409	Abp31409 Human ORF	631	7	2.4	145	3	AAU23380	Aau23380 Yeast AGA
559	8	2.8	131	4	AAU25812	Aau25812 Human pro	632	7	2.4	153	5	ABU51699	Abu51699 Helicobac
560	8	2.8	138	4	AAU75945	Aau75945 Human col	633	7	2.4	161	5	ABO05752	Abo05752 Human G p
561	8	2.8	150	3	AAU57885	Aau57885 Human tra	634	7	2.4	167	3	AAU43143	Aau43143 Arabidops
562	8	2.8	195	3	AAU94680	Aau94680 Human pro	635	7	2.4	167	3	AAU15570	Aau15570 Arabidops
563	8	2.8	200	4	AAE02640	Aae02640 Human DNA	636	7	2.4	175	4	ABG03484	Abg03484 Novel hum
564	8	2.8	292	5	AAO19224	Aao19224 Human IRC	637	7	2.4	185	6	ABU37668	Abu37668 Protein e
565	8	2.8	298	2	AAU24023	Aau24023 Human CMR	638	7	2.4	185	6	ABU37260	Abu37260 Protein e
566	8	2.8	298	7	ADD18704	Add18704 Human dis	639	7	2.4	208	6	ABP80476	Abp80476 N. gonorr
567	8	2.8	301	2	AAU24022	Aau24022 Human CMR	640	7	2.4	208	6	ABP79656	Abp79656 N. gonorr
568	8	2.8	313	4	AAE02639	Aae02639 Human DNA	641	7	2.4	217	4	AAU53543	Aau53543 Propionib
569	8	2.8	461	7	ADC64559	Adc64559 Trichodes	642	7	2.4	217	6	ABM50062	Abm50062 C. elegan
570	8	2.8	472	6	ABB82660	Abb82660 N. puncti	643	7	2.4	218	3	AAU65681	Aau65681 C. elegan
571	8	2.8	475	6	ADC64556	Adc64556 Nostoc pu	644	7	2.4	229	4	AAU04888	Aau04888 Micromono
572	8	2.8	475	6	ABB82659	Abb82659 Anabaena	645	7	2.4	235	4	ABR00941	AbR00941 Gene 216
573	8	2.8	475	7	ADC64555	Adc64555 Anabaena	646	7	2.4	235	6	ABR57160	AbR57160 Human p10
574	7	2.4	29	6	AAO27002	Aao27002 Human NGR	647	7	2.4	235	6	ABU55869	Abu55869 Human gen
575	7	2.4	24	3	AAU54386	Aau54386 Amino aci	648	7	2.4	236	6	ABR00939	AbR00939 Gene 216
576	7	2.4	30	3	AAU54395	Aau54395 Amino aci	649	7	2.4	236	6	ABU55867	Abu55867 Human gen
577	7	2.4	31	3	AAU54387	Aau54387 Amino aci	650	7	2.4	255	4	ABG06508	Abg06508 Novel hum
578	7	2.4	31	3	AAU54388	Aau54388 Amino aci	651	7	2.4	257	6	ABO07794	Abo07794 Allolococ
579	7	2.4	31	3	AAU54396	Aau54396 Amino aci	652	7	2.4	266	4	AAU63702	Aau63702 Human gas
580	7	2.4	32	3	AAU54389	Aau54389 Amino aci	653	7	2.4	276	4	AAU63704	Aau63704 Human gas
581	7	2.4	32	3	AAU54405	Aau54405 Amino aci	654	7	2.4	286	3	AAU21001	Aau21001 Arabidops
582	7	2.4	32	3	AAU54397	Aau54397 Amino aci	655	7	2.4	299	3	AAU52488	Aau52488 Helicobac
583	7	2.4	33	2	AAU74959	Aau74959 Human sec	656	7	2.4	299	5	ABU51909	Abu51909 Helicobac
584	7	2.4	33	3	AAU54390	Aau54390 Amino aci	657	7	2.4	302	4	ABR00940	AbR00940 Gene 216
585	7	2.4	33	3	AAU54406	Aau54406 Amino aci	658	7	2.4	302	6	ABU55868	Abu55868 Human gen
586	7	2.4	33	3	AAU54398	Aau54398 Amino aci	659	7	2.4	309	6	ABJ18975	Abj18975 Staphyloc
587	7	2.4	33	5	ABG95419	Abg95419 Human nov	660	7	2.4	309	6	ABU50836	Abu50836 Helicobac
588	7	2.4	33	6	ABO34613	Abo34613 Region of	661	7	2.4	311	5	AAU78884	Aau78884 Human pro
589	7	2.4	34	3	AAU54391	Aau54391 Amino aci	662	7	2.4	312	4	AAW72349	Aaw72349 Staphyloc
590	7	2.4	34	3	AAU54399	Aau54399 Amino aci	663	7	2.4	312	6	ABP75549	Abp75549 Human sec
591	7	2.4	34	3	AAU54407	Aau54407 Amino aci	664	7	2.4	313	6	ABP75549	Abp75549 Human sec
592	7	2.4	35	3	AAU54400	Aau54400 Amino aci	665	7	2.4	319	5	ABU55009	Abu55009 Lactococc
593	7	2.4	35	3	AAU54408	Aau54408 Amino aci	666	7	2.4	331	2	AAU42332	Aau42332 Staphyloc
594	7	2.4	36	3	AAU54409	Aau54409 Amino aci	667	7	2.4	331	2	AAU42332	Aau42332 Staphyloc
595	7	2.4	42	3	AAU28732	Aau28732 Human sec	668	7	2.4	331	2	AAU42332	Aau42332 Staphyloc
596	7	2.4	50	5	AAU63141	Aau63141 Propionib	669	7	2.4	331	2	AAU42332	Aau42332 Staphyloc
597	7	2.4	50	5	ABP34982	Abp34982 Human ORF	670	7	2.4	340	4	AAU78883	Aau78883 Human pro
598	7	2.4	50	6	ABM59660	Abm59660 Propionib	671	7	2.4	361	6	AAO30434	Aao30434 Human glu
599	7	2.4	59	4	AAE08114	Aae08114 Human gen	672	7	2.4	361	6	ABO07796	Abo07796 Allolococ
600	7	2.4	59	5	ABG33936	Abg33936 Human sec	673	7	2.4	361	7	ADD46622	Add46622 Human PRO
601	7	2.4	60	3	AAU87137	Aau87137 Human sec	674	7	2.4	363	3	ABU52168	Abu52168 Human sec
602	7	2.4	60	4	AAU01640	Aau01640 Human sec	675	7	2.4	373	3	ADC97421	Adc97421 E. faeculi
603	7	2.4	92	1	AAU93591	Aau93591 Deduced s	676	7	2.4	388	2	AAU25698	Aau25698 Murine ad
604	7	2.4	92	2	AAU01805	Aau01805 Murine ma	677	7	2.4	391	6	ABO00918	Abo00918 Polypepti
605	7	2.4	92	2	AAU42166	Aau42166 Rat MTPI-	678	7	2.4	400	2	AAU32501	Aau32501 Beta-adre
606	7	2.4	106	5	AAU52436	Aau52436 HIV_Nef1	679	7	2.4	400	2	AAU54992	Aau54992 Murine be
607	7	2.4	107	2	AAU70792	Aau70792 Melanoma	680	7	2.4	400	2	ADD47841	Add47841 Rat Prote
608	7	2.4	107	2	AAU96713	Aau96713 Growth re	681	7	2.4	406	3	AAU21000	Aau21000 Arabidops
609	7	2.4	107	3	AAU15793	Aau15793 Human che	682	7	2.4	422	4	AAU882216	Aau882216 Megalomic

683	7	2.4	430	3	AAG20999	Arabidops	756	7	2.4	704	4	AAB82620	Mouse sub
684	7	2.4	434	6	ABU20683	Protein e	757	7	2.4	744	4	AAg78648	Human Rai
685	7	2.4	440	4	ABE59628	Drosophil	758	7	2.4	746	2	AAW80322	Bacillus
686	7	2.4	441	4	AAW79867	Human pro	759	7	2.4	756	6	ABU39148	Protein e
687	7	2.4	441	4	AAW79868	Human pro	760	7	2.4	759	2	AAW46864	Bacillus
688	7	2.4	441	6	AAO27001	Human NGR	761	7	2.4	759	2	AAy24967	Bacillus
689	7	2.4	448	4	AAW60715	Human bra	762	7	2.4	769	5	ABP68905	Human pol
690	7	2.4	448	4	ABG55105	Human liv	763	7	2.4	769	7	ADSB64492	Human pro
691	7	2.4	448	5	ABG43242	Human pep	764	7	2.4	787	3	ADD43705	Bacillus
692	7	2.4	449	6	AAO19850	B licheni	765	7	2.4	787	3	AAy59284	SUP toxin
693	7	2.4	449	6	AAO19851	B licheni	766	7	2.4	787	6	ABE82567	B. thurin
694	7	2.4	470	4	AAU01085	Gene 7 Hu	767	7	2.4	787	6	ABE82565	B. thurin
695	7	2.4	477	4	ABR94878	Human pro	768	7	2.4	787	7	ADD43701	Bacillus
696	7	2.4	477	4	ABR94726	Human pro	769	7	2.4	788	7	ADC07798	Rice prot
697	7	2.4	477	5	AAE15741	Human aml	770	7	2.4	788	7	ADD43703	Bacillus
698	7	2.4	478	6	ABU18317	Protein e	771	7	2.4	789	2	AAy91244	B. thurin
699	7	2.4	491	5	AAU84364	Novel hum	772	7	2.4	789	2	AAy91243	B. thurin
700	7	2.4	506	5	ABU51515	Helicobac	773	7	2.4	789	2	AAW19514	B. cereus
701	7	2.4	509	1	ABP91060	Predicted	774	7	2.4	789	2	AAW19514	B. cereus
702	7	2.4	511	2	AAW46865	Bacillus	775	7	2.4	789	2	AAW80321	Bacillus
703	7	2.4	511	2	AAy24968	Bacillus	776	7	2.4	789	2	AAW80320	Bacillus
704	7	2.4	514	5	ABP70073	Human NOV	777	7	2.4	789	2	AAW60216	Bacillus
705	7	2.4	519	2	AAy35553	Protein i	778	7	2.4	789	2	AAW60217	Bacillus
706	7	2.4	521	2	AAy27808	Bovine he	779	7	2.4	789	2	AAW46726	Native ve
707	7	2.4	521	2	AAy41344	Bovine he	780	7	2.4	789	2	AAW46725	Vegetativ
708	7	2.4	521	2	AAy77400	BHVI gIII	781	7	2.4	789	2	AAW46862	Bacillus
709	7	2.4	524	4	AAy31600	Amino aci	782	7	2.4	789	2	AAW46870	Bacillus
710	7	2.4	524	5	ABO9661	Amino aci	783	7	2.4	789	2	AAW46863	Bacillus
711	7	2.4	524	5	ABO9663	Amino aci	784	7	2.4	789	2	AAW46868	Bacillus
712	7	2.4	530	4	AAE64386	Amino aci	785	7	2.4	789	2	AAW46867	Bacillus
713	7	2.4	533	4	AAE96234	Putative	786	7	2.4	789	2	AAW46869	Bacillus
714	7	2.4	547	4	ABE68141	Drosophil	787	7	2.4	789	2	AAW46866	Bacillus
715	7	2.4	560	7	ADD48908	Rat Prote	788	7	2.4	789	2	AAW46861	Bacillus
716	7	2.4	561	5	ABE57090	Mouse isc	789	7	2.4	789	2	AAy24971	Bacillus
717	7	2.4	564	2	AAE28413	Prod. of	790	7	2.4	789	2	AAy24966	Bacillus
718	7	2.4	564	2	AAE69733	Cyclic-GM	791	7	2.4	789	2	AAy24970	Bacillus
719	7	2.4	564	2	AAW11257	Heart cal	792	7	2.4	789	2	AAy24974	Bacillus
720	7	2.4	564	2	AAW18041	Human hea	793	7	2.4	789	2	AAy24972	Bacillus
721	7	2.4	564	2	AAW1229	Human 61	794	7	2.4	789	2	AAy24965	Bacillus
722	7	2.4	564	2	AAW77045	Human hea	795	7	2.4	789	2	AAy24964	Bacillus
723	7	2.4	564	2	AAW60757	Amino aci	796	7	2.4	789	2	AAy24973	Bacillus
724	7	2.4	564	3	AAy80990	Human 61	797	7	2.4	789	2	AAy24969	Bacillus
725	7	2.4	564	6	ABU58729	Human 61k	798	7	2.4	789	6	ABE82566	B. thurin
726	7	2.4	569	4	ABG13053	Novel hum	799	7	2.4	790	2	AAW60215	Bacillus
727	7	2.4	579	4	AAy93285	Human pro	800	7	2.4	790	2	AAW46872	Bacillus
728	7	2.4	580	5	ABE97409	Novel hum	801	7	2.4	790	2	AAW46871	Bacillus
729	7	2.4	580	5	ABE89675	Human A10	802	7	2.4	790	2	AAy24975	Bacillus
730	7	2.4	599	7	ADC31234	Human nov	803	7	2.4	796	2	AAy11896	Toxin fro
731	7	2.4	614	2	AAW20991	H. pylori	804	7	2.4	796	5	ABP68904	Human pol
732	7	2.4	623	4	AAy92236	C glutami	805	7	2.4	801	4	ABG82463	S. epide
733	7	2.4	625	4	AAy79455	Corynebac	806	7	2.4	801	6	ABU42569	Protein e
734	7	2.4	633	4	ABG07544	Novel hum	807	7	2.4	801	6	ABU42569	Protein e
735	7	2.4	634	2	AAE28412	Prod. cDN	808	7	2.4	808	5	ABP38260	Staphyloc
736	7	2.4	634	2	AAE69732	Cyclic-GM	809	7	2.4	808	2	AAy91261	VIP3(a)
737	7	2.4	634	2	AAW11256	Hippocamp	810	7	2.4	809	2	AAW19521	B. cereus
738	7	2.4	634	2	AAW18040	Human bra	811	7	2.4	809	2	AAW46732	Maize opt
739	7	2.4	634	2	AAW71228	Human 61	812	7	2.4	812	4	AAW46732	Maize opt
740	7	2.4	634	2	AAW77044	Ca2+/calm	813	7	2.4	812	4	ABr07106	Second sp
741	7	2.4	634	2	AAW60756	Amino aci	814	7	2.4	812	5	ABR00942	Gene 216
742	7	2.4	634	3	AAy80989	Human 61	815	7	2.4	812	5	ABR78300	Amino aci
743	7	2.4	634	6	ABU58728	Human 61k	816	7	2.4	812	5	AAO14377	Human met
744	7	2.4	634	7	ADE54788	Rat Prote	817	7	2.4	812	6	AAU98885	Human pro
745	7	2.4	634	7	ADE54792	Rat Prote	818	7	2.4	813	4	ABU55870	Human 216
746	7	2.4	635	2	AAW75855	Human sec	819	7	2.4	813	6	ABU58632	Human PRO
747	7	2.4	635	2	AAy45160	Human sec	820	7	2.4	813	6	ABU58632	Human PRO
748	7	2.4	635	3	AAy71060	Human mem	821	7	2.4	813	6	ABU88180	Novel hum
749	7	2.4	635	6	ABP97203	Tumour-as	822	7	2.4	813	6	ABU88180	Novel hum
750	7	2.4	635	7	ADE54790	Human Pro	823	7	2.4	813	6	ABR66369	Human sec
751	7	2.4	635	7	ADE54794	Human Pro	824	7	2.4	813	6	ABR66369	Human sec
752	7	2.4	651	4	ABG06511	Novel hum	825	7	2.4	813	6	ABU99699	Human sec
753	7	2.4	652	4	ABE59286	Drosophil	826	7	2.4	813	6	ABU82338	Human PRO
754	7	2.4	661	4	ABE59862	Drosophil	827	7	2.4	813	6	ABU90059	Novel hum
755	7	2.4	686	5	AAO14360	Human met	828	7	2.4	813	6	ABU68308	Human sec
												ABU96361	Novel hum

829	7	2.4	813	6	ABU92792	Human sec	902	7	2.4	813	6	ABO00024	Novel hum
830	7	2.4	813	6	ABO08869	Human sec	903	7	2.4	813	6	ABR66674	Human sec
831	7	2.4	813	6	ABO02921	Human sec	904	7	2.4	813	6	ABR91092	Human sec
832	7	2.4	813	6	ABR75075	Human sec	905	7	2.4	813	6	ABU94519	Human PRO
833	7	2.4	813	6	ABR94837	Human PRO	906	7	2.4	813	6	ABU79401	Human PRO
834	7	2.4	813	6	ABU85810	Human PRO	907	7	2.4	813	6	ABU86730	Human sec
835	7	2.4	813	6	ABU98970	Novel hum	908	7	2.4	813	6	ABU87035	Novel hum
836	7	2.4	813	6	ABU98185	Novel hum	909	7	2.4	813	6	ABU84824	Human PRO
837	7	2.4	813	6	ABU91891	Novel hum	910	7	2.4	813	6	ABO04751	Human PRO
838	7	2.4	813	6	ABU98584	Human PRO	911	7	2.4	813	6	ABR70500	Human sec
839	7	2.4	813	6	ABU86425	Human sec	912	7	2.4	813	6	ABU98665	Human PRO
840	7	2.4	813	6	ABU67638	Human sec	913	7	2.4	813	6	ABR66064	Human sec
841	7	2.4	813	6	ABU80666	Human PRO	914	7	2.4	813	6	ABR64781	Human sec
842	7	2.4	813	6	ABR99584	Human sec	915	7	2.4	813	6	ABU79706	Human PRO
843	7	2.4	813	6	ABR98974	Human sec	916	7	2.4	813	6	ABU93097	Human sec
844	7	2.4	813	6	ABO16497	Human sec	917	7	2.4	813	6	ABU96056	Human PRO
845	7	2.4	813	6	ABR92397	Human sec	918	7	2.4	813	6	ABU91276	Novel hum
846	7	2.4	813	6	ABO19038	Human sec	919	7	2.4	813	6	ABU90369	Novel hum
847	7	2.4	813	6	ABR78459	Human sec	920	7	2.4	813	6	ABO09784	Human sec
848	7	2.4	813	6	ABU85195	Novel hum	921	7	2.4	813	6	ABO11056	Human sec
849	7	2.4	813	6	ABO00334	Novel hum	922	7	2.4	813	6	ABR71110	Human sec
850	7	2.4	813	6	ABO11666	Human sec	923	7	2.4	813	6	ABU87718	Human PRO
851	7	2.4	813	6	ABO02311	Human sec	924	7	2.4	813	6	ABU91586	Human PRO
852	7	2.4	813	6	ABU88885	Novel hum	925	7	2.4	813	6	ABU84800	Human sec
853	7	2.4	813	6	ABU83580	Human sec	926	7	2.4	813	6	ABR69890	Human sec
854	7	2.4	813	6	ABO06381	Novel hum	927	7	2.4	813	6	ABU80267	Human PRO
855	7	2.4	813	6	ABR59437	Human sec	928	7	2.4	813	6	ABU93536	Human PRO
856	7	2.4	813	6	ABO09479	Human sec	929	7	2.4	813	6	ABO10089	Human sec
857	7	2.4	813	6	ABO19343	Novel hum	930	7	2.4	813	6	ABO09174	Human sec
858	7	2.4	813	6	ABO11361	Human sec	931	7	2.4	813	6	ABU10742	Human sec
859	7	2.4	813	6	ABR66979	Human sec	932	7	2.4	813	6	ABU95751	Human PRO
860	7	2.4	813	6	ABO16192	Human sec	933	7	2.4	813	6	ABU96960	Novel hum
861	7	2.4	813	6	ABO13898	Human sec	934	7	2.4	813	6	ABR70805	Human sec
862	7	2.4	813	6	ABU65801	Human sec	935	7	2.4	813	6	ABO05156	Novel hum
863	7	2.4	813	6	ABO07649	Human PRO	936	7	2.4	813	6	ABO08564	Human sec
864	7	2.4	813	6	ABO03836	Human sec	937	7	2.4	813	6	ABO05771	Human sec
865	7	2.4	813	6	ABR67284	Human sec	938	7	2.4	813	6	ABR74160	Human sec
866	7	2.4	813	6	ABO15887	Human sec	939	7	2.4	813	6	ABR95752	Human sec
867	7	2.4	813	6	ABU56168	Human sec	940	7	2.4	813	6	ABR81049	Human sec
868	7	2.4	813	6	ABU65496	Human PRO	941	7	2.4	813	6	ABR81354	Human sec
869	7	2.4	813	6	ABU95441	Novel hum	942	7	2.4	813	6	ABM01050	Human sec
870	7	2.4	813	6	ABU71344	Human PRO	943	7	2.4	813	6	ABR88652	Human sec
871	7	2.4	813	6	ABO07954	Human PRO	944	7	2.4	813	6	ABM77473	Human sec
872	7	2.4	813	6	ABR70195	Human sec	945	7	2.4	813	6	ABO28957	Human sec
873	7	2.4	813	6	ABR69528	Human sec	946	7	2.4	813	6	ABO31702	Human sec
874	7	2.4	813	6	ABO01669	Human PRO	947	7	2.4	813	6	ABM08119	Human sec
875	7	2.4	813	6	ABU81471	Human PRO	948	7	2.4	813	6	ABO40599	Human sec
876	7	2.4	813	6	ABR60268	Human sec	949	7	2.4	813	6	ABO36024	Human PRO
877	7	2.4	813	6	ABR68003	Human sec	950	7	2.4	813	6	ABO44163	Human PRO
878	7	2.4	813	6	ABR65391	Human sec	951	7	2.4	813	6	ADA78218	Human sec
879	7	2.4	813	6	ABR68613	Human sec	952	7	2.4	813	6	ABM24958	Human sec
880	7	2.4	813	6	ABR72025	Human sec	953	7	2.4	813	6	ABO03226	Human sec
881	7	2.4	813	6	ABU95505	Human PRO	954	7	2.4	813	6	ABR90482	Human sec
882	7	2.4	813	6	ABU89195	Human sec	955	7	2.4	813	6	ABM17396	Human sec
883	7	2.4	813	6	ABU83275	Human sec	956	7	2.4	813	6	ABR95142	Human sec
884	7	2.4	813	6	ABU95131	Novel hum	957	7	2.4	813	6	ABR95447	Human sec
885	7	2.4	813	6	ABU90679	Novel hum	958	7	2.4	813	6	ABO21685	Human sec
886	7	2.4	813	6	ABU94190	Human sec	959	7	2.4	813	6	ABR97949	Human sec
887	7	2.4	813	6	ABU93841	Novel hum	960	7	2.4	813	6	ABR87737	Human sec
888	7	2.4	813	6	ABR65086	Human sec	961	7	2.4	813	6	ABM77778	Human sec
889	7	2.4	813	6	ABR68918	Human sec	962	7	2.4	813	6	ABM28008	Human sec
890	7	2.4	813	6	ABO06734	Human sec	963	7	2.4	813	6	ABM06289	Human sec
891	7	2.4	813	6	ABR99279	Human sec	964	7	2.4	813	6	ABM03795	Human sec
892	7	2.4	813	6	ABU57163	Human PRO	965	7	2.4	813	6	ABM35246	Human sec
893	7	2.4	813	6	ABU86115	Novel hum	966	7	2.4	813	6	ABM26483	Human sec
894	7	2.4	813	6	ABU82402	Novel hum	967	7	2.4	813	6	ABO48265	Human sec
895	7	2.4	813	6	ABU87413	Human PRO	968	7	2.4	813	6	ABR93007	Human sec
896	7	2.4	813	6	ABU83885	Human sec	969	7	2.4	813	6	ABO24768	Human sec
897	7	2.4	813	6	ABO08259	Human PRO	970	7	2.4	813	6	ABM11779	Human sec
898	7	2.4	813	6	ABU81970	Novel hum	971	7	2.4	813	6	ABM02680	Human sec
899	7	2.4	813	6	ABU66134	Novel hum	972	7	2.4	813	6	ABM16176	Human sec
900	7	2.4	813	6	ABR59963	Human sec	973	7	2.4	813	6	ABO27737	Human sec
901	7	2.4	813	6	ABU94151	Novel hum	974	7	2.4	813	6	ABM29228	Human sec

PF 14-AUG-2000; 2000WO-US022315.
XX 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn ME, Lu DAM, Patterson C;
XX WPI; 2001-168860/17.
DR N-PSDB; AAF81758.
XX Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX Claim 1; Page 131-132; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated with
CC MEMAP
XX
SQ Sequence 290 AA;
Query Match 57.2%; Score 166; DB 4; Length 290;
Best Local Similarity 99.68; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPLLTLVLLFWLSGYSIAQTGPTTVNGLERSLTVQCVYRSGWETYLKWWCRGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIAQTGPTTVNGLERSLTVQCVYRSGWETYLKWWCRGAIWR 60
Qy 61 DCKLVKTSGEQVKEKDRYSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
Db 61 DCKLVKTSGEQVKEKDRYSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
Qy 121 VQVTDIPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180
Db 121 VQVTDIPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180
Qy 181 MKYQQAAGMSPEVLOPLEGDIYADLTLOLAGTSRKAATKLSSAQVQVEVEYVYMA 240
Db 181 MKYQQAAGMSPEVLOPLEGDIYADLTLOLAGTSRKAATKLSSAQVQVEVEYVYMA 240
Qy 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
RESULT 3
ID AAU83611 standard; protein; 290 AA.
XX

AC AAU83611;
XX 08-MAY-2002 (first entry)
XX Human PRO protein, Seq ID No 40.
DE
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX WO200208288-A2.
PN 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253648P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Deanoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
DR N-PSDB; ABR33555.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 11; Fig 40; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumors, especially lung
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
CC liver tumor. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have

CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU8392-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 5; Length 290;
 Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDIMKTDADTYWCGIEKTNGLGVT 120
 Db 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDIMKTDADTYWCGIEKTNGLGVT 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 4

ABU80758
 ID ABU80758 standard; protein; 290 AA.

XX AC ABU80758;
 XX DT 23-JUN-2003 (first entry)
 XX DE Human PRO polypeptide #20.
 XX KW Human; PRO polypeptide; secreted and transmembrane protein;
 XX KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
 XX OS Homo sapiens.
 XX FN US2003036635-A1.
 XX PD 20-FEB-2003.
 XX PF 28-AUG-2002; 2002US-00230163.
 XX PR 25-JUN-2000; 2000US-0220638P.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-342045/32.
 XX DR N-PSDB; ACA66860.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 XX useful for the manufacture of a medicament for diagnosing or treating
 XX tumor.

XX Claim 11; Fig 40; 314pp; English.

XX The present invention relates to the isolation of novel human PRO
 XX polypeptides, and the polynucleotide sequences encoding them. The PRO

CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
 CC useful in diagnostic assays for PRO, by detecting its expression in
 CC specific cells, tissues or serum, and for affinity purification of PRO
 CC from recombinant cell culture or natural sources. ABU80739-ABU80860
 CC represent the human PRO polypeptides of the invention. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov/psipdidentry.html

XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
 Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDIMKTDADTYWCGIEKTNGLGVT 120
 Db 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDIMKTDADTYWCGIEKTNGLGVT 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 5

ABO33724
 ID ABO33724 standard; protein; 290 AA.

XX AC ABO33724;
 XX DT 17-SEP-2003 (first entry)
 XX DE Novel human secreted and transmembrane protein PRO10111.
 XX KW Human; secreted and transmembrane protein; PRO; cytostatic;
 XX KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
 XX KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
 XX KW pharmaceutical; diagnostic; biosensor; bioeffector; tumour; lung tumour;
 XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX KW liver tumour; bone disorder; cartilage disorder; sports injury;
 XX KW arthritis; wound.
 XX OS Homo sapiens.
 XX FN US2003045687-A1.
 XX PD 06-MAR-2003.
 XX PF 12-AUG-2002; 2002US-00218631.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-512315/48.

DR N-PSDB; ACD68612.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.
 XX
 XX
 PS Claim 11; Fig 40; 314pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;
 Query Match 57.2%; Score 166; DB 6; Length 290;
 Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEGEVQRDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 Db 61 DCKILVKTSGSEGEVQRDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLQPLEGDLGYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQQAAGMSPEQVLQPLEGDLGYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEQDQPTTCNMG 267
 Db 241 SLPKEDISYASLTGAEQDQPTTCNMG 267
 RESULT 6
 ABUS2067
 ID ABUS2067 standard; protein; 290 AA.
 XX
 AC ABUS2067;
 XX
 DT 25-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW

KW antiangiogenic; hypotensive; vulnentry; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
 XX
 XX Homo sapiens.
 OS
 XX US2003088063-A1.
 FN
 XX 08-MAY-2003.
 PD
 XX 12-AUG-2002; 2002US-00219003.
 PF
 XX 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US0217800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-393229/37.
 DR N-PSDB; ACA68516.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 40; 314pp; English.
 XX
 CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;
 Query Match 57.2%; Score 166; DB 6; Length 290;
 Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEGEVQRDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 Db 61 DCKILVKTSGSEGEVQRDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLQPLEGDLGYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQQAAGMSPEQVLQPLEGDLGYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEQDQPTTCNMG 267
 Db 241 SLPKEDISYASLTGAEQDQPTTCNMG 267

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RESULT 7
ABJ72247
ID ABJ72247 standard; protein; 290 AA.
XX
XX
AC ABJ72247;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10111 protein.
XX
KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003050448-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230414.
XX
XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI
DR WPI; 2003-521818/49.
DR N-PSDB; APT44245.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX
XX Claim 11; Fig 40; 315pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of chondrocyte proliferation or
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
CC protein of the invention
XX
XX Sequence 290 AA;
XX
Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPILLTLLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPILLTLLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLVGT 120
QY 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIILLVLAASLAWRM 180
Db 121 VQVITDPAVPTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIILLVLAASLAWRM 180
QY 181 MKYQQKAAGMSPEQLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240

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Db 181 MKYQQKAAGMSPEQLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTTCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTTCNMG 267
XX
XX
XX
XX 06-NOV-2003 (first entry)
XX
XX Human PRO10111 protein.
XX
XX PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
XX Homo sapiens.
XX
XX US2003027988-A1.
XX
XX 06-FEB-2003.
XX
XX 26-AUG-2002; 2002US-00227884.
XX
XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI
DR WPI; 2003-503301/47.
DR N-PSDB; APT44528.
XX
XX New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
XX Claim 11; Fig 40; 324pp; English.
XX
XX The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
XX Sequence 290 AA;
XX
Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPILLTLLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPILLTLLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGLVGT 120

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QY 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 DB 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGLGAEDQEPTCYNMG 267
 DB 241 SLPKEDISYASLTGLGAEDQEPTCYNMG 267
 RESULT 9
 ABO34270
 ID ABO34270 standard; protein; 290 AA.
 AC ABO34270;
 XX
 DT 19-SEP-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO 10111.
 XX
 KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
 KW human dermal fibroblast stimulation; tumour; tissue typing;
 KW affinity purification.
 XX
 OS Homo sapiens.
 XX
 XX US2003044934-A1.
 PN
 XX
 PD 06-MAR-2003.
 XX
 XX 28-AUG-2002; 2002US-00230338.
 PF
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-492274/46.
 DR N-PSDB; ACD82195.
 XX
 XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, or in generating probes.
 XX
 PS Claim 19; Fig 40; 315pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. Nucleic acids that encode PRO can be used to generate either
 CC transgenic animals or knock-out animals useful in developing and
 CC screening of therapeutically useful reagents. The nucleic acids may also
 CC be used in gene therapy for replacing defective gene, in chromosome
 CC identification, as chromosome markers, or in generating probes to isolate
 CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
 CC stimulation. TNF-alpha stimulation, human dermal fibroblasts stimulation
 CC and for detecting the presence of tumour in an mammal. The PRO
 CC polypeptides are useful as molecular markers for protein electrophoresis
 CC and the isolated nucleic acids may be used for recombinantly expressing
 CC those markers. The PRO polypeptides and nucleic acids may also be used in
 CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
 CC PRO and in affinity purification of PRO from recombinant cell culture or
 CC natural sources. The present sequence represents the amino acid sequence
 CC of a human secreted/transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;
 Query Match 57.2%; Score 166; DB 6; Length 290;

Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MELLTLYLLFWLSGYSIATQITPTTVNGLERGLTVQCVRSGWETYLKWWCRGAIWR 60
 DB 1 MELLTLYLLFWLSGYSIATQITPTTVNGLERGLTVQCVRSGWETYLKWWCRGAIWR 60
 QY 61 DCKTLVKTSSSEORVEDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 DB 61 DCKTLVKTSSSEORVEDRYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 DB 121 VQVTIDPAPVTOBETSSPTLGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGLGAEDQEPTCYNMG 267
 DB 241 SLPKEDISYASLTGLGAEDQEPTCYNMG 267
 RESULT 10
 ABJ72077
 ID ABJ72077 standard; protein; 290 AA.
 XX ABJ72077;
 AC ABJ72077;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE Human membrane bound receptor/protein PRO10111 amino acid sequence.
 XX
 KW Human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuroepithelial; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX
 OS Homo sapiens.
 XX
 XX US2003065147-A1.
 PN
 XX
 PD 03-APR-2003.
 XX
 XX 29-AUG-2002; 2002US-00232224.
 PF
 XX
 PR 28-JUL-1999; 99US-0146222P.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-522018/49.
 DR N-PSDB; ABT43901.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for the manufacture of a medicament for diagnosing or treating
 PT tumor.
 XX
 PS Claim 11; Fig 40; 315pp; English.
 XX
 CC This invention relates to one hundred and twenty two novel nucleic acids
 CC encoding human PRO membrane bound proteins or receptors. Extracellular
 CC proteins play important roles in the formation, differentiation and
 CC maintenance of multicellular organisms. The fate of many individual cells

(for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neurotrophic factors and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention

Query Match 57.2%; Score 166; DB 7; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPELLTLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60

Qy 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

Qy 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180

Qy 181 MKYQKKAAGSPQVLOPLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVYMA 240
Db 181 MKYQKKAAGSPQVLOPLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVYMA 240

Qy 241 SLPKEDISYASLTGAEQDQPTVCNMG 267
Db 241 SLPKEDISYASLTGAEQDQPTVCNMG 267

RESULT 11
ID ADB83530 standard; protein; 290 AA.
AC ADB83530;
XX ADB83530;
XX 04-DEC-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO1011.
XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX Homo sapiens.
XX US2003073814-A1.
XX 17-APR-2003.
XX 12-AUG-2002; 2002US-00218849.

01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
(GETH) GENENTECH INC.
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
N-PSDB; ADB83529.
WP1; 2003-644806/61.
New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
Claim 11; Fig 40; 315pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO836, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567, PRO1887, PRO1928, PRO1341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO5723, PRO5725, PRO7154 or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc., are useful for detecting the presence of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 290 AA;
Query Match 57.2%; Score 166; DB 7; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPELLTLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTLLYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60

Qy 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

Qy 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180

Qy 181 MKYQKKAAGSPQVLOPLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVYMA 240

Db 181 MKYQQAAGSPQVLPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISVASLTGAEDEQPTVCNMG 267
 Db 241 SLPKEDISVASLTGAEDEQPTVCNMG 267
 RESULT 12
 ADB80636
 ID ADB80636 standard; protein; 290 AA.
 XX ADB80636;
 AC ADB80636;
 XX 04-DEC-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO10111.
 XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2003088068-A1.
 XX 08-MAY-2003.
 XX 13-AUG-2002; 2002US-00219481.
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-657982/62.
 DR N-PSDB; ADB80635.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX Claim 11; Fig 40; 305pp; English.
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO155, PRO1306 or PRO419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO419, PRO214,
 CC PRO247, PRO337, PRO526, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1487, PRO1428, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 7; Length 290;
 Best Local Similarity 99.6%; Pred.No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSGLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKDRVSIKQNKRPPTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 Db 61 DCKILVKTSGSEQEVKDRVSIKQNKRPPTVTMEDLMKTDADTYWCGIEKTDGLGVT 120
 QY 121 VQVVIDPAPVTQETSSPTLTGHHLDNRHKLKLVLLPLFTIIXLLLVAAALLAWRM 180
 Db 121 VQVVIDPAPVTQETSSPTLTGHHLDNRHKLKLVLLPLFTIIXLLLVAAALLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQQAAGMSPEQVLPLEGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISVASLTGAEDEQPTVCNMG 267
 Db 241 SLPKEDISVASLTGAEDEQPTVCNMG 267

RESULT 13
 ADB73177
 ID ADB73177 standard; protein; 290 AA.
 XX ADB73177;
 AC ADB73177;
 XX 04-DEC-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO10111.
 XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2003096968-A1.
 XX 22-MAY-2003.
 XX 29-AUG-2002; 2002US-00232223.
 XX 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI, 2003-765525/72.
 DR N-PSDB; ADB73176.
 XX New isolated PRO polypeptides useful as molecular weight markers in
 PT protein electrophoresis, useful for tissue typing, and for treating
 PT arthritis and tumors.
 XX Claim 11; Fig 40; 308pp; English.
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO846, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX SQ Sequence 290 AA;
 Query Match 57.2%; Score 166; DB 7; Length 290;
 Best Local Similarity 99.68; Pred. No. 3.e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MPLLTLVLLFLWLSGYSIATQITGPTVNGLRSGLTVQCVYRSGMETHYKWCRAINR 60
 Db 1 MPLLTLVLLFLWLSGYSIATQITGPTVNGLRSGLTVQCVYRSGMETHYKWCRAINR 60
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 Db 61 DCKLIVKTSQSEQRKDRYSIKDNQKRNRTFTVMDLMTKTDADTWCGTEKGNLDLGV 120
 Qy 121 VQVITDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLFTIILLIVAAASLLAWRM 180
 Db 121 VQVITDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLFTIILLIVAAASLLAWRM 180
 Qy 181 MKYQKAGMSPEQVQLFEGDLCLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQKAGMSPEQVQLFEGDLCLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Qy 241 SLPKEDISYASLTILGAEDQDEPTCYNMG 267
 Db 241 SLPKEDISYASLTILGAEDQDEPTCYNMG 267
 RESULT 14
 ADB78259
 ID ADB78259 standard; protein; 290 AA.
 XX
 AC ADB78259;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 OS US2003092889-A1.
 PN
 XX 15-MAY-2003.
 PF
 XX 13-AUG-2002; 2002US-00219478.
 PR
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI, 2003-765495/72.
 DR N-PSDB; ADB78258.
 XX
 XX New isolated PRO polypeptide useful for tissue typing, gene therapy, as
 PT molecular weight markers in protein electrophoresis, and for treating
 PT arthritis and tumors.
 XX
 PS Claim 11; Fig 40; 308pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO846, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,

CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.

XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 7; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERSLTVCQVRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERSLTVCQVRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOBETSSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180
DB 121 VQVTTIDPAPVTOBETSSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLQPLEGDLQVADLTQLAGTSFRKATTKLSSAQVDQVEVEYVTA 240
DB 181 MKYQQAAGMSPEQVLQPLEGDLQVADLTQLAGTSFRKATTKLSSAQVDQVEVEYVTA 240

QY 241 SLPKEDISASLTGAEDQDEPTCYNMG 267

DB 241 SLPKEDISASLTGAEDQDEPTCYNMG 267

RESULT 15

ADB84907

ID ADB84907 standard; protein; 290 AA.

XX AC ADB84907;

XX DT 04-DEC-2003 (first entry)

XX DE Human PRO polypeptide #20.

XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
XX cancer; lung; colon; breast; prostate; rectum; liver;
XX tumour necrosis factor- α ; TNF- α ; blood; chondrocyte cell;
XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
XX arthritis; sports injury; cytostatic; antiarthritic.

XX OS Homo sapiens.

XX FN US2003073817-A1.

XX PD 17-APR-2003.

XX PF 26-AUG-2002; 2002US-00227883.

XX PR 01-AUG-2000; 2000US-0222425P.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-730024/69.

DR N-PSDB; ADB84906.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful

PT e.g. in gene therapy, disease diagnosis, chromosome identification and

PT tissue typing.

XX Claim 11; Fig 40; 314pp; English.

XX The invention relates to human PRO polypeptides (secreted and

CC transmembrane polypeptides) and the PRO polynucleotides encoding them.

CC The PRO polypeptides and polynucleotides are useful as Pharmaceuticals,

CC diagnostics, biosensors or bioreactors. They are particularly useful for

CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,

CC prostate tumour, rectal tumour or liver tumour) in a mammal, for

CC stimulating the release of tumour necrosis factor (TNF)- α from human

CC blood, for stimulating the proliferation or differentiation of

CC chondrocyte cells, for stimulating the proliferation of or gene

CC expression in pericyte cells or for stimulating the proliferation of

CC normal human dermal fibroblasts. The PRO nucleic acids are useful as

CC hybridisation probes, in chromosome and gene mapping, in generating

CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant

CC technology, in generating transgenic animals or knock-out animals which

CC may be used in the development and screening of therapeutically useful

CC reagents, in gene therapy, in chromosome identification, as chromosome

CC markers and in generating probes. The PRO polypeptides, or anti-PRO

CC antibodies, are useful for preparing a medicament for treating a

CC condition which is responsive to the PRO polypeptides or anti-PRO

CC antibodies, such as pericyte-associated tumours and bone and/or cartilage

CC disorders (e.g. arthritis, sports injuries), involving inducing the re-

CC differentiation of chondrocytes. The PRO polypeptides are useful as

CC molecular markers for protein electrophoresis, and in tissue typing. This

CC sequence represents a human PRO polypeptide of the invention.

XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 7; Length 290;

Best Local Similarity 99.6%; Pred. No. 3.3e-155;

Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERSLTVCQVRSGWETYLKWCRCGAIWR 60

DB 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERSLTVCQVRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

DB 61 DCKILVKTSGEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTTIDPAPVTOBETSSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180

DB 121 VQVTTIDPAPVTOBETSSSPTLTGHLDNRHKLKLSVLLPLFTIIXLLLVAAASLLAWRM 180

QY 181 MKYQQAAGMSPEQVLQPLEGDLQVADLTQLAGTSFRKATTKLSSAQVDQVEVEYVTA 240

DB 181 MKYQQAAGMSPEQVLQPLEGDLQVADLTQLAGTSFRKATTKLSSAQVDQVEVEYVTA 240

QY 241 SLPKEDISASLTGAEDQDEPTCYNMG 267

DB 241 SLPKEDISASLTGAEDQDEPTCYNMG 267

Search completed: September 16, 2004, 12:55:08

Job time : 167 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:51:52 : Search time 32 Seconds

(without alignments)
467.860 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290

Sequence: 1 MFLITLTLFWLGVSIAT.....SXLPGRGPETPEYSTISRP 290

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Gapop 60.0 , Capext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	10	3.4	195	3	US-08-955-937A-4
2	10	3.4	195	3	US-09-300-985-4
3	10	3.4	201	3	US-08-955-937A-2
4	10	3.4	201	3	US-09-300-985-2
5	8	2.8	107	1	US-08-352-324A-4
6	8	2.8	107	2	US-08-862-607-4
7	8	2.8	107	2	US-08-468-819-6
8	8	2.8	107	3	US-09-203-235-4
9	8	2.8	107	4	US-09-213-383-6
10	8	2.8	107	5	PCT-US95-16144-4
11	8	2.8	298	4	US-09-582-934-2
12	8	2.8	301	4	US-09-582-934-1
13	7	2.4	29	3	US-09-348-578-4
14	7	2.4	29	4	US-09-699-684-4
15	7	2.4	30	1	US-08-087-772A-9
16	7	2.4	30	3	US-09-348-578-5
17	7	2.4	30	3	US-09-699-684-5
18	7	2.4	30	4	US-09-699-684-5
19	7	2.4	30	4	US-09-699-684-13
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21	7	2.4	31	3	US-09-348-578-14
22	7	2.4	31	3	US-09-348-578-22
23	7	2.4	31	4	US-09-699-684-6
24	7	2.4	31	4	US-09-699-684-14
25	7	2.4	31	4	US-09-699-684-22
26	7	2.4	32	3	US-09-348-578-7
27	7	2.4	32	3	US-09-348-578-15

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54	7	2.4	92	4	US-09-771-023-11	Sequence 11, Appl
55	7	2.4	106	4	US-08-679-493A-148	Sequence 148, App
56	7	2.4	107	1	US-08-352-324A-7	Sequence 7, Appl
57	7	2.4	107	2	US-08-862-607-7	Sequence 7, Appl
58	7	2.4	107	2	US-08-468-819-5	Sequence 5, Appl
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61	7	2.4	107	5	PCT-US95-16144-7	Sequence 7, Appl
62	7	2.4	145	3	US-08-808-599A-41	Sequence 41, Appl
63	7	2.4	218	4	US-09-084-303B-204	Sequence 204, App
64	7	2.4	309	1	US-08-723-202-1	Sequence 1, Appl
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67	7	2.4	344	4	US-09-252-991A-31786	Sequence 31786, A
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69	7	2.4	373	4	US-09-107-532A-7048	Sequence 7048, Ap
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139 7 2.4 789 3 US-09-402-036-2 Sequence 4, Appl
140 7 2.4 789 3 US-09-402-036-4 Sequence 80, Appl
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242 6 2.1 91 4 US-08-134-001C-5262 Sequence 5262, Ap
243 6 2.1 92 4 US-08-732-210-1515 Sequence 1515, Ap
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250	6	2.1	103	2	US-08-448-561-4	Sequence 4, Appl	323	6	2.1	197	2	US-08-855-261A-1	Sequence 1, Appl
251	6	2.1	104	2	US-08-616-392C-12	Sequence 12, Appl	324	6	2.1	197	4	US-09-227-224-1	Sequence 1, Appl
252	6	2.1	110	4	US-09-149-476-593	Sequence 593, Ap	325	6	2.1	197	4	US-08-855-288-1	Sequence 1, Appl
253	6	2.1	110	4	US-09-547-435-22	Sequence 22, Appl	326	6	2.1	198	4	US-09-227-357-232	Sequence 232, Ap
254	6	2.1	112	4	US-08-858-207A-125	Sequence 125, Ap	327	6	2.1	198	4	US-09-800-170-25	Sequence 25, Appl
255	6	2.1	113	3	US-09-345-041-138	Sequence 138, Ap	328	6	2.1	199	4	US-09-800-170-28	Sequence 28, Appl
256	6	2.1	114	4	US-09-107-532A-5394	Sequence 5394, Ap	329	6	2.1	202	4	US-08-679-493A-197	Sequence 197, Ap
257	6	2.1	116	3	US-08-545-809A-92	Sequence 92, Appl	330	6	2.1	206	4	US-08-205-258-463	Sequence 463, Ap
258	6	2.1	116	3	US-08-545-809A-118	Sequence 118, Ap	331	6	2.1	206	4	US-09-107-532A-6952	Sequence 6952, Ap
259	6	2.1	116	3	US-08-545-809A-140	Sequence 140, Ap	332	6	2.1	206	4	US-09-540-236-3153	Sequence 3153, Ap
260	6	2.1	116	4	US-09-462-917A-22	Sequence 22, Appl	333	6	2.1	210	4	US-09-134-001C-4065	Sequence 4065, Ap
261	6	2.1	116	4	US-09-328-352-7417	Sequence 7417, Ap	334	6	2.1	210	4	US-09-252-991A-30886	Sequence 30886, A
262	6	2.1	117	3	US-08-545-809A-114	Sequence 114, Ap	335	6	2.1	217	4	US-08-679-493A-196	Sequence 196, Ap
263	6	2.1	117	3	US-09-489-039A-12399	Sequence 12399, A	336	6	2.1	218	3	US-08-113-750A-9	Sequence 9, Appl
264	6	2.1	118	3	US-08-545-809A-116	Sequence 116, Ap	337	6	2.1	220	1	US-08-225-989-19	Sequence 19, Appl
265	6	2.1	118	3	US-08-545-809A-123	Sequence 123, Ap	338	6	2.1	220	1	US-08-570-923-19	Sequence 19, Appl
266	6	2.1	118	3	US-08-545-809A-142	Sequence 142, Ap	339	6	2.1	220	1	US-08-580-014-19	Sequence 19, Appl
267	6	2.1	120	3	US-08-545-809A-137	Sequence 137, Ap	340	6	2.1	220	3	US-09-079-785-19	Sequence 19, Appl
268	6	2.1	121	4	US-09-352-991A-26954	Sequence 26954, A	341	6	2.1	220	4	US-09-628-126-19	Sequence 19, Appl
269	6	2.1	125	4	US-09-134-001C-5034	Sequence 5034, Ap	342	6	2.1	221	4	US-08-679-493A-198	Sequence 198, Ap
270	6	2.1	126	2	US-08-561-521-2	Sequence 2, Appl	343	6	2.1	221	4	US-08-874-926-2	Sequence 2, Appl
271	6	2.1	126	2	US-08-561-521-15	Sequence 15, Appl	344	6	2.1	222	4	US-08-384-162-8	Sequence 8, Appl
272	6	2.1	126	4	US-09-107-532A-7133	Sequence 7133, Ap	345	6	2.1	234	4	US-09-543-681A-4712	Sequence 4712, Ap
273	6	2.1	126	5	PCT-US95-01219-2	Sequence 2, Appl	346	6	2.1	236	4	US-09-252-991A-29709	Sequence 29709, A
274	6	2.1	126	5	PCT-US95-01219-15	Sequence 15, Appl	347	6	2.1	239	1	US-08-235-989-6	Sequence 6, Appl
275	6	2.1	128	1	US-08-339-582-4	Sequence 4, Appl	348	6	2.1	239	1	US-08-570-923-6	Sequence 6, Appl
276	6	2.1	130	2	US-08-944-449-2	Sequence 2, Appl	349	6	2.1	239	1	US-08-580-014-6	Sequence 6, Appl
277	6	2.1	130	4	US-09-353-362-2	Sequence 2, Appl	350	6	2.1	239	3	US-08-079-785-6	Sequence 6, Appl
278	6	2.1	130	4	US-09-489-039A-13887	Sequence 13887, A	351	6	2.1	239	4	US-09-921-667-4	Sequence 4, Appl
279	6	2.1	131	1	US-08-441-629-6	Sequence 6, Appl	352	6	2.1	239	4	US-08-628-126-6	Sequence 6, Appl
280	6	2.1	131	3	US-08-776-207-6	Sequence 6, Appl	353	6	2.1	241	4	US-09-328-352-8001	Sequence 8001, Ap
281	6	2.1	131	4	US-09-507-773-6	Sequence 6, Appl	354	6	2.1	241	4	US-09-543-681A-5245	Sequence 5245, Ap
282	6	2.1	131	5	PCT-US95-09172-6	Sequence 6, Appl	355	6	2.1	248	4	US-09-252-991A-23110	Sequence 23110, A
283	6	2.1	132	2	US-08-616-392C-10	Sequence 6, Appl	356	6	2.1	253	4	US-09-543-681A-6581	Sequence 6581, Ap
284	6	2.1	132	4	US-08-635-109-1	Sequence 1, Appl	357	6	2.1	256	4	US-08-232-412-2	Sequence 2, Appl
285	6	2.1	133	4	US-09-352-991A-29953	Sequence 29953, A	358	6	2.1	257	4	US-08-205-258-233	Sequence 233, Ap
286	6	2.1	134	4	US-09-621-976-3902	Sequence 3902, Ap	359	6	2.1	257	4	US-09-489-039A-13129	Sequence 13129, A
287	6	2.1	137	4	US-09-149-476-393	Sequence 393, Ap	360	6	2.1	257	4	US-09-134-000C-6129	Sequence 6129, Ap
288	6	2.1	139	1	US-08-478-039-108	Sequence 108, Ap	361	6	2.1	258	2	US-08-847-900-4	Sequence 4, Appl
289	6	2.1	139	1	US-08-476-349A-108	Sequence 108, Ap	362	6	2.1	264	4	US-09-107-532A-4581	Sequence 4581, Ap
290	6	2.1	139	3	US-08-523-894-2	Sequence 2, Appl	363	6	2.1	264	4	US-09-489-039A-10454	Sequence 10454, A
291	6	2.1	139	4	US-09-347-435-18	Sequence 18, Appl	364	6	2.1	270	2	US-08-773-368-1	Sequence 1, Appl
292	6	2.1	139	4	US-09-347-435-18	Sequence 18, Appl	365	6	2.1	270	3	US-09-199-887-1	Sequence 1, Appl
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295	6	2.1	142	3	US-08-908-643C-53	Sequence 53, Appl	368	6	2.1	275	4	US-09-107-532A-5237	Sequence 5237, Ap
296	6	2.1	142	3	US-08-847-065-21	Sequence 21, Appl	369	6	2.1	275	4	US-09-134-000C-6042	Sequence 6042, Ap
297	6	2.1	147	4	US-09-252-991A-22087	Sequence 22087, A	370	6	2.1	278	4	US-09-149-476-454	Sequence 454, Ap
298	6	2.1	148	4	US-09-621-976-3957	Sequence 3957, Ap	371	6	2.1	278	4	US-09-543-681A-5811	Sequence 5811, Ap
299	6	2.1	150	4	US-09-621-976-4059	Sequence 4059, Ap	372	6	2.1	278	4	US-09-134-000C-5311	Sequence 5311, Ap
300	6	2.1	151	2	US-08-722-050-8	Sequence 8, Appl	373	6	2.1	281	4	US-09-512-251A-9	Sequence 9, Appl
301	6	2.1	151	4	US-09-883-985-8	Sequence 8, Appl	374	6	2.1	281	4	US-09-515-150A-9	Sequence 12, Appl
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303	6	2.1	155	4	US-09-800-170-54	Sequence 54, Appl	376	6	2.1	285	4	US-09-252-991A-23332	Sequence 23332, A
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305	6	2.1	157	4	US-09-540-236-3731	Sequence 3731, Ap	378	6	2.1	289	4	US-09-252-991A-23564	Sequence 23564, A
306	6	2.1	159	4	US-09-205-258-615	Sequence 615, Ap	379	6	2.1	291	4	US-09-547-435-14	Sequence 14, Appl
307	6	2.1	161	4	US-09-252-991A-22676	Sequence 22676, A	380	6	2.1	292	4	US-09-651-200-16	Sequence 16, Appl
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310	6	2.1	166	3	US-08-908-643C-51	Sequence 51, Appl	383	6	2.1	292	4	US-09-543-681A-5561	Sequence 5561, Ap
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312	6	2.1	170	4	US-09-328-352-8037	Sequence 8037, Ap	385	6	2.1	294	4	US-09-540-236-2814	Sequence 2814, Ap
313	6	2.1	173	4	US-09-252-991A-27863	Sequence 27863, A	386	6	2.1	296	1	US-08-261-662-2	Sequence 2, Appl
314	6	2.1	174	2	US-08-683-262B-59	Sequence 59, Appl	387	6	2.1	296	5	PCT-US95-07752-2	Sequence 2, Appl
315	6	2.1	174	3	US-09-361-707-59	Sequence 59, Appl	388	6	2.1	300	4	US-09-794-960-5	Sequence 5, Appl
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317	6	2.1	174	4	US-09-489-039A-12363	Sequence 12363, A	390	6	2.1	304	4	US-09-489-039A-14181	Sequence 14181, A
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319	6	2.1	178	4	US-09-252-991A-23820	Sequence 23820, A	392	6	2.1	311	1	US-08-118-270-37	Sequence 37, Appl

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394	6	2.1	312	4	US-09-252-991A-23610	Sequence 23610, A	467	6	2.1	429	4	US-09-372-425A-6	Sequence 6, Appl
395	6	2.1	313	4	US-09-543-681A-4278	Sequence 4278, Ap	468	6	2.1	429	4	US-09-328-352-4643	Sequence 4643, Ap
396	6	2.1	316	4	US-09-759-281B-1	Sequence 1, Appl	469	6	2.1	431	4	US-09-800-170-1	Sequence 1, Appl
397	6	2.1	319	4	US-09-358-383C-22	Sequence 22, Appl	470	6	2.1	431	4	US-09-543-681A-6326	Sequence 6326, Ap
398	6	2.1	321	4	US-09-582-660-5	Sequence 5, Appl	471	6	2.1	431	4	US-09-543-681A-7623	Sequence 7623, Ap
399	6	2.1	324	4	US-09-489-039A-12945	Sequence 12945, A	472	6	2.1	433	4	US-09-252-991A-2548	Sequence 2548, A
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402	6	2.1	333	4	US-09-107-532A-4988	Sequence 4988, Ap	475	6	2.1	434	4	US-09-800-170-48	Sequence 48, Appl
403	6	2.1	334	4	US-09-252-991A-20310	Sequence 20310, A	476	6	2.1	437	4	US-09-800-170-49	Sequence 49, Appl
404	6	2.1	334	4	US-09-489-039A-9328	Sequence 9328, Ap	477	6	2.1	438	4	US-09-800-170-30	Sequence 30, Appl
405	6	2.1	338	1	US-08-218-686-2	Sequence 2, Appl	478	6	2.1	438	4	US-09-800-170-32	Sequence 32, Appl
406	6	2.1	338	4	US-08-460-242-2	Sequence 2, Appl	479	6	2.1	438	4	US-09-800-170-34	Sequence 34, Appl
407	6	2.1	338	4	US-09-325-932A-60	Sequence 60, Appl	480	6	2.1	438	4	US-09-800-170-36	Sequence 36, Appl
408	6	2.1	340	4	US-09-134-001C-3258	Sequence 3258, Ap	481	6	2.1	438	4	US-09-800-170-38	Sequence 38, Appl
409	6	2.1	342	4	US-09-489-039A-8662	Sequence 8662, Ap	482	6	2.1	438	4	US-09-800-170-40	Sequence 40, Appl
410	6	2.1	355	4	US-09-252-991A-18900	Sequence 18900, A	483	6	2.1	438	4	US-09-800-170-42	Sequence 42, Appl
411	6	2.1	359	4	US-09-134-001C-4842	Sequence 4842, Ap	484	6	2.1	438	4	US-09-800-170-44	Sequence 44, Appl
412	6	2.1	359	4	US-09-266-965-120	Sequence 120, App	485	6	2.1	438	4	US-09-800-170-46	Sequence 46, Appl
413	6	2.1	360	4	US-09-252-991A-17420	Sequence 17420, A	486	6	2.1	438	4	US-09-489-039A-8527	Sequence 8527, Ap
414	6	2.1	362	4	US-09-134-001C-5403	Sequence 5403, Ap	487	6	2.1	441	4	US-09-543-681A-7207	Sequence 7207, Ap
415	6	2.1	365	4	US-09-328-352-6517	Sequence 6517, Ap	488	6	2.1	441	4	US-09-610-006-1	Sequence 4669, Ap
416	6	2.1	369	4	US-09-489-039A-7587	Sequence 7587, Ap	489	6	2.1	441	4	US-09-134-000C-4669	Sequence 1, Appl
417	6	2.1	375	4	US-09-489-039A-9807	Sequence 9807, Ap	490	6	2.1	444	4	US-09-489-039A-10922	Sequence 10922, A
418	6	2.1	376	2	US-08-933-750C-25	Sequence 25, Appl	491	6	2.1	444	4	US-08-660-451A-12	Sequence 12, Appl
419	6	2.1	376	2	US-09-234-613-25	Sequence 25, Appl	492	6	2.1	446	4	US-08-107-532A-5776	Sequence 5776, Ap
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422	6	2.1	378	4	US-09-325-932A-158	Sequence 158, App	495	6	2.1	450	3	US-09-071-434-1	Sequence 1, Appl
423	6	2.1	383	1	US-08-230-448A-78	Sequence 78, Appl	496	6	2.1	450	3	US-09-413-814-101	Sequence 101, Appl
424	6	2.1	383	1	US-08-230-448A-78	Sequence 78, Appl	497	6	2.1	454	3	US-09-109-204-1	Sequence 1, Appl
425	6	2.1	383	1	US-08-175-069A-78	Sequence 78, Appl	498	6	2.1	454	3	US-09-430-032-1	Sequence 1, Appl
426	6	2.1	383	4	US-08-461-939B-78	Sequence 78, Appl	499	6	2.1	457	2	US-08-847-900-3	Sequence 3, Appl
427	6	2.1	384	4	US-08-464-000-78	Sequence 78, Appl	500	6	2.1	457	2	US-08-847-900-3	Sequence 3, Appl
428	6	2.1	384	4	US-09-489-039A-13733	Sequence 13733, A	501	6	2.1	458	2	US-08-655-878-2	Sequence 2, Appl
429	6	2.1	386	4	US-09-820-005-2	Sequence 2, Appl	502	6	2.1	458	2	US-08-489-039A-13954	Sequence 13954, A
430	6	2.1	388	4	US-09-215-450-24	Sequence 24, Appl	503	6	2.1	462	4	US-09-328-352-6888	Sequence 6888, Ap
431	6	2.1	390	4	US-08-620-005-4	Sequence 4, Appl	504	6	2.1	462	4	US-09-907-794A-285	Sequence 285, Ap
432	6	2.1	393	3	US-08-888-429A-21	Sequence 21, Appl	505	6	2.1	463	4	US-09-905-125A-285	Sequence 285, App
433	6	2.1	393	4	US-09-533-653-21	Sequence 21, Appl	506	6	2.1	463	4	US-09-902-775A-285	Sequence 285, App
434	6	2.1	397	4	US-09-252-991A-20668	Sequence 3, Appl	507	6	2.1	466	4	US-09-292-097-15	Sequence 15, Appl
435	6	2.1	401	3	US-09-517-802-3	Sequence 3, Appl	508	6	2.1	466	4	US-09-252-991A-26545	Sequence 26545, A
436	6	2.1	401	4	US-09-252-991A-17272	Sequence 17272, A	509	6	2.1	467	3	US-08-523-894-8	Sequence 8, Appl
437	6	2.1	402	4	US-09-252-991A-26529	Sequence 26529, A	510	6	2.1	467	3	US-08-523-894-10	Sequence 10, Appl
438	6	2.1	403	4	US-09-489-039A-11877	Sequence 11877, A	511	6	2.1	467	3	US-08-523-894-12	Sequence 12, Appl
439	6	2.1	408	4	US-09-252-991A-25757	Sequence 25757, A	512	6	2.1	469	4	US-09-332-041-3	Sequence 3, Appl
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443	6	2.1	417	4	US-09-328-352-4168	Sequence 4168, Ap	516	6	2.1	473	3	US-09-049-672A-4	Sequence 4, Appl
444	6	2.1	421	2	US-08-576-826A-53	Sequence 53, Appl	517	6	2.1	473	3	US-09-134-001C-3564	Sequence 3564, Ap
445	6	2.1	422	4	US-08-634-238-226	Sequence 226, App	518	6	2.1	474	4	US-09-489-039A-13282	Sequence 13282, A
446	6	2.1	425	1	US-07-657-769B-69	Sequence 69, Appl	519	6	2.1	475	4	US-09-252-991A-30242	Sequence 30242, A
447	6	2.1	425	1	US-08-097-938-7	Sequence 7, Appl	520	6	2.1	476	3	US-08-487-550-4	Sequence 4, Appl
448	6	2.1	425	1	US-07-789-184-220	Sequence 220, App	521	6	2.1	476	3	US-08-487-550-12	Sequence 12, Appl
449	6	2.1	425	1	US-08-476-000-7	Sequence 7, Appl	522	6	2.1	476	3	US-09-526-098-4	Sequence 4, Appl
450	6	2.1	425	1	US-08-475-263-220	Sequence 220, App	523	6	2.1	476	4	US-09-526-098-12	Sequence 12, Appl
451	6	2.1	425	1	US-08-472-840-7	Sequence 7, Appl	524	6	2.1	476	4	US-09-252-991A-30304	Sequence 30304, A
452	6	2.1	425	1	US-08-485-886-220	Sequence 220, App	525	6	2.1	479	4	US-09-543-681A-6605	Sequence 6605, Ap
453	6	2.1	425	2	US-08-477-362-220	Sequence 220, App	526	6	2.1	480	3	US-09-537-357-32	Sequence 32, Appl
454	6	2.1	425	2	US-08-477-134-220	Sequence 3, Appl	527	6	2.1	480	3	US-09-537-357-32	Sequence 32, Appl
455	6	2.1	425	2	US-08-911-320A-3	Sequence 3, Appl	528	6	2.1	481	4	US-09-252-991A-31708	Sequence 31708, A
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457	6	2.1	425	2	US-08-742-440A-7	Sequence 7, Appl	530	6	2.1	483	2	US-08-686-599A-5	Sequence 5, Appl
458	6	2.1	425	2	US-08-50-088A-57	Sequence 57, Appl	531	6	2.1	483	2	US-08-686-599A-16	Sequence 16, Appl
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460	6	2.1	425	3	US-08-474-410-7	Sequence 7, Appl	533	6	2.1	493	2	US-09-134-001C-4475	Sequence 4475, Ap
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464	6	2.1	425	3	US-08-486-673B-7	Sequence 7, Appl	537	6	2.1	502	2	US-08-700-636-8	Sequence 8, Appl
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544	6	2.1	502	US-09-892-985-8	Sequence 8, Appli	617	6	2.1	686	US-09-245-041-13	Sequence 13, Appli
545	6	2.1	502	US-09-954-936-2	Sequence 2, Appli	618	6	2.1	690	US-09-198-452A-1068	Sequence 1068, Ap
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553	6	2.1	516	US-09-345-473B-34	Sequence 34, Appli	626	6	2.1	714	US-09-422-869-22	Sequence 22, Appli
554	6	2.1	523	US-09-489-039A-9202	Sequence 9202, Ap	627	6	2.1	714	US-09-308-345A-47	Sequence 47, Appli
555	6	2.1	526	US-08-311-731A-291	Sequence 291, App	628	6	2.1	715	US-09-134-000C-5094	Sequence 5094, Ap
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557	6	2.1	529	US-09-976-594-958	Sequence 958, App	630	6	2.1	727	US-09-179-558-56	Sequence 56, Appli
558	6	2.1	534	US-09-134-000C-4924	Sequence 4924, Ap	631	6	2.1	727	US-09-722-825-56	Sequence 56, Appli
559	6	2.1	538	US-09-205-258-343	Sequence 343, App	632	6	2.1	727	US-09-722-487-56	Sequence 56, Appli
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564	6	2.1	557	US-08-793-229-33	Sequence 33, Appli	637	6	2.1	741	US-08-434-998-2	Sequence 2, Appli
565	6	2.1	557	US-09-285-957-33	Sequence 33, Appli	638	6	2.1	741	US-08-434-998-4	Sequence 4, Appli
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568	6	2.1	564	US-09-489-039A-14047	Sequence 14047, A	641	6	2.1	741	US-08-701-005A-2	Sequence 2, Appli
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570	6	2.1	571	US-09-711-164-406	Sequence 406, App	643	6	2.1	741	US-08-943-956A-2	Sequence 2, Appli
571	6	2.1	572	US-09-328-352-4176	Sequence 4176, Ap	644	6	2.1	741	PCT-US95-02058-2	Sequence 2, Appli
572	6	2.1	575	US-09-786-240-14	Sequence 14, Appli	645	6	2.1	741	PCT-US95-02058-4	Sequence 4, Appli
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575	6	2.1	578	US-09-489-039A-10599	Sequence 10599, A	648	6	2.1	769	US-09-543-681A-7175	Sequence 7175, Ap
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577	6	2.1	581	US-09-221-928-8	Sequence 8, Appli	650	6	2.1	771	US-09-634-238-262	Sequence 262, App
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585	6	2.1	581	US-09-221-237-8	Sequence 8, Appli	658	6	2.1	816	US-09-496-672-53	Sequence 53, Appli
586	6	2.1	581	US-09-799-875-11	Sequence 11, Appli	659	6	2.1	837	US-09-122-126B-2	Sequence 2, Appli
587	6	2.1	583	US-08-616-392C-4	Sequence 4, Appli	660	6	2.1	837	US-09-634-286A-2	Sequence 2, Appli
588	6	2.1	584	US-09-252-991A-24311	Sequence 24311, A	661	6	2.1	837	US-09-252-991A-30713	Sequence 30713, A
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590	6	2.1	595	US-09-640-419C-20	Sequence 20, Appli	663	6	2.1	844	US-08-541-780-6	Sequence 94, Appli
591	6	2.1	600	US-08-253-785-3	Sequence 3, Appli	664	6	2.1	845	US-08-804-439A-94	Sequence 94, Appli
592	6	2.1	607	US-08-752-307B-12	Sequence 12, Appli	665	6	2.1	845	US-09-720-229-94	Sequence 94, Appli
593	6	2.1	607	US-09-707-802-12	Sequence 12, Appli	666	6	2.1	846	US-07-731-157A-5	Sequence 5, Appli
594	6	2.1	607	US-09-991-326-12	Sequence 12, Appli	667	6	2.1	846	US-08-541-780-5	Sequence 5, Appli
595	6	2.1	609	US-09-252-991A-25487	Sequence 25487, A	668	6	2.1	867	US-09-547-435-24	Sequence 24, Appli
596	6	2.1	611	US-09-543-681A-5447	Sequence 5447, Ap	669	6	2.1	872	US-08-844-057-2	Sequence 2, Appli
597	6	2.1	612	US-09-252-991A-31248	Sequence 31248, A	670	6	2.1	872	US-09-006-730-2	Sequence 2, Appli
598	6	2.1	618	US-09-252-991A-22418	Sequence 22418, A	671	6	2.1	879	US-09-252-991A-31990	Sequence 31990, A
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602	6	2.1	638	US-09-413-814-102	Sequence 102, App	675	6	2.1	895	US-09-614-912-194	Sequence 194, App
603	6	2.1	638	US-09-252-991A-25205	Sequence 25205, A	676	6	2.1	908	US-08-487-890A-94	Sequence 94, Appli
604	6	2.1	641	US-09-543-681A-4453	Sequence 4453, Ap	677	6	2.1	908	US-08-478-435-94	Sequence 94, Appli
605	6	2.1	646	US-09-252-991A-16819	Sequence 16819, A	678	6	2.1	908	US-08-337-483-94	Sequence 94, Appli
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607	6	2.1	647	US-09-489-039A-8388	Sequence 8388, Ap	680	6	2.1	908	US-08-474-671-94	Sequence 94, Appli
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611	6	2.1	673	US-09-252-991A-26458	Sequence 26458, A	684	6	2.1	908	US-08-897-438-94	Sequence 94, Appli

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691	6	2.1	908	4	US-08-753-750B-12	Sequence 12, Appl	764	4	US-08-980-357-28	Sequence 15, Appl
692	6	2.1	908	2	US-08-363-124A-4	Sequence 4, Appl	765	4	US-08-198-446B-15	Sequence 15, Appl
693	6	2.1	913	1	US-08-445-640-4	Sequence 4, Appl	766	4	US-08-870-693-15	Sequence 42, Appl
694	6	2.1	913	3	US-08-170-558-4	Sequence 4, Appl	767	4	US-09-058-489-35	Sequence 35, Appl
695	6	2.1	913	3	US-08-447-314-4	Sequence 4, Appl	768	4	US-09-245-041-15	Sequence 15, Appl
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700	6	2.1	925	5	PCT-US94-14893-1	Sequence 1, Appl	773	4	US-08-652-877-86	Sequence 86, Appl
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703	6	2.1	932	4	US-09-071-035-416	Sequence 416, App	776	4	US-08-437-013-23	Sequence 23, Appl
704	6	2.1	938	4	US-09-252-991A-23882	Sequence 23882, A	777	4	US-09-360-237-37	Sequence 37, Appl
705	6	2.1	941	3	US-08-179-558-55	Sequence 55, Appl	778	4	US-09-275-506A-23	Sequence 23, Appl
706	6	2.1	941	4	US-09-722-825-55	Sequence 55, Appl	779	4	US-08-340-428B-31	Sequence 31, Appl
707	6	2.1	941	4	US-09-722-825-55	Sequence 55, Appl	780	4	US-08-519-180-1	Sequence 1, Appl
708	6	2.1	941	4	US-09-722-825-55	Sequence 55, Appl	781	4	US-08-519-180-1	Sequence 1, Appl
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711	6	2.1	962	4	US-08-939-106-6	Sequence 6, Appl	784	4	US-09-460-384-3	Sequence 3, Appl
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753	6	2.1	1422	4	US-08-477-344A-81	Sequence 81, Appl	826	4	US-08-465-325-94	Sequence 94, Appl
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843	5	1.7	11	3	US-09-115-737-94	Sequence 94, Appl	916	5	1.7	15	4	US-09-391-270-33	Sequence 33, Appl
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871	5	1.7	13	1	US-08-434-120-97	Sequence 97, Appl	944	5	1.7	16	5	PCT-US94-07019-11	Sequence 11, Appl
872	5	1.7	13	1	US-08-465-325-96	Sequence 96, Appl	945	5	1.7	16	5	PCT-US94-07019-12	Sequence 12, Appl
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876	5	1.7	13	4	US-09-115-737-96	Sequence 96, Appl	949	5	1.7	17	1	US-07-725-331-51	Sequence 51, Appl
877	5	1.7	14	1	US-08-193-521-4	Sequence 4, Appl	950	5	1.7	17	1	US-07-725-331-55	Sequence 55, Appl
878	5	1.7	14	1	US-08-434-120-98	Sequence 98, Appl	951	5	1.7	17	1	US-07-725-331-56	Sequence 56, Appl
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887	5	1.7	14	5	PCT-US94-07019-8	Sequence 8, Appl	960	5	1.7	17	4	US-09-316-919-55	Sequence 55, Appl
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ALIGNMENTS

RESULT 1
US-08-955-937A-4
; Sequence 4, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-955-937A-4
Query Match 3.4%; Score 10; DB 3; Length 195;
Best Local Similarity 100.0%; Pred.No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 DRVSIKDNQK 87
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Db 74 DRVSIKDNQK 83
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RESULT 2
US-09-300-985-4
; Sequence 4, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
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; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (122) (170) (184)
US-09-300-985-4
Query Match 3.4%; Score 10; DB 3; Length 195;
Best Local Similarity 100.0%; Pred.No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 DRVSIKDNQK 87
|||||
Db 74 DRVSIKDNQK 83
|||||
RESULT 3
US-08-955-937A-2
; Sequence 2, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-937A-2

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Query Match      3.4%; Score 10; DB 3; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      78 DRVSIKDQK 87
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```
Db      74 DRVSIKDQK 83
```

RESULT 4

```

US-09-300-985-2
; Sequence 2, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEWSEGED
; APPLICANT: HUBLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 201
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-300-985-2

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Query Match      3.4%; Score 10; DB 3; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```
Qy      78 DRVSIKDQK 87
```

```
Db      74 DRVSIKDQK 83
```

RESULT 5

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US-08-352-324A-4
; Sequence 4, Application US/08352324A
; Patent No. 5633149
; GENERAL INFORMATION:

```

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; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,324A
; FILING DATE: 07-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-352-324A-4

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Query Match      2.8%; Score 8; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      167 LLLVVAAS 174
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Db      22 LLLVVAAS 29
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RESULT 6

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US-08-862-607-4
; Sequence 4, Application US/08862607
; Patent No. 5844084
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/862,607
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-862-607-4

Query Match      2.8%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 LLLVVAAS 174
Db      22 LLLVVAAS 29

RESULT 7
US-08-468-819-6
; Sequence 6, Application US/08468819
; Patent No. 5871723
; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
; APPLICANT: Polverini, Peter J.
; APPLICANT: Kunkel, Steven L.
; TITLE OF INVENTION: CXG Chemokines as Regulators of
; TITLE OF INVENTION: CXG Chemokines as Regulators of
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC-003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; APPLICATION NUMBER: US/08/862,607
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-203-235-4

Query Match      2.8%; Score 8; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 LLLVVAAS 174
Db      22 LLLVVAAS 29

RESULT 8
US-09-203-235-4
; Sequence 4, Application US/09203235
; Patent No. 6071701
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/203,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,607
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-203-235-4

Query Match      2.8%; Score 8; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 LLLVVAAS 174
Db      22 LLLVVAAS 29

RESULT 9
US-09-213-383-6
; Sequence 6, Application US/09213383
; Patent No. 6491906
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; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
; Polverini, Peter J.
; Kunkel, Steven L.
; TITLE OF INVENTION: CXC Chemokines as Regulators of
; Angiogenesis
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,383
; FILING DATE: 09-Dec-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-213-383-6

Query Match 2.8%; Score 8; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 10
PCT-US95-16144-4
; Sequence 4, Application PC/TUS9516144
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFLAMED
; TISSUE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1/MS-DOS 6.2

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16144
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,324
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0025 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-16144-4

Query Match 2.8%; Score 8; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 11
US-09-582-934-2
; Sequence 2, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-2

Query Match 2.8%; Score 8; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 ASLLAWRM 180
Db 195 ASLLAWRM 202

RESULT 12
US-09-582-934-1
; Sequence 1, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM

```

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; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:we really don't
; OTHER INFORMATION: know
US-09-582-934-1

Query Match      2.8%; Score 8; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 11;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      173 ASLLAWRM 180
Db      195 ASLLAWRM 202
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RESULT 13
US-09-348-578-4
; Sequence 4, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA secretion
; OTHER INFORMATION: signal
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-09-348-578-4

Query Match      2.4%; Score 7; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      167 LLLLVAA 173
Db      9 LLLLVAA 15
|||||

RESULT 14
US-09-699-684-4
; Sequence 4, Application US/09699684
; Patent No. 6436674
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu

```

```

; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/699,684
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/348,578
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA secretion
; OTHER INFORMATION: signal
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-09-699-684-4

Query Match      2.4%; Score 7; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      167 LLLLVAA 173
Db      9 LLLLVAA 15
|||||

RESULT 15
US-08-087-772A-9
; Sequence 9, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-087-772A-9

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Query Match 2.4%; Score 7; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 275 GCGPEEP 281
| | | | |
Db 4 GCGPEEP 10

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Job time : 44 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:57:08 ; Search time 129 Seconds
(without alignments)
721.928 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 290
Sequence: 1 MFLTLYLLFWLSGYSIAT.....SXLPGRGPEPTETYSIRP 290

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- 6: /cgn2_6/ptodata1/pubpaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
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561	10	3.4	201	14	US-10-205-508-608	Sequence 608, App	634	10	3.4	201	15	US-10-195-900-608	Sequence 608, App
562	10	3.4	201	14	US-10-205-905-608	Sequence 608, App	635	10	3.4	201	15	US-10-198-759-608	Sequence 608, App
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567	10	3.4	201	14	US-10-223-090-344	Sequence 344, App	640	10	3.4	201	15	US-10-207-915-608	Sequence 608, App
568	10	3.4	201	14	US-10-223-087-344	Sequence 608, App	641	10	3.4	201	16	US-10-197-709-608	Sequence 608, App
569	10	3.4	201	14	US-10-198-760-608	Sequence 608, App	642	10	3.4	201	16	US-10-206-916-608	Sequence 608, App
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571	10	3.4	201	14	US-10-184-613-608	Sequence 608, App	644	9	3.1	623	14	US-10-289-757-166	Sequence 166, Appl
572	10	3.4	201	14	US-10-187-739-608	Sequence 608, App	645	9	3.1	1102	12	US-10-289-757-67	Sequence 67, Appl
573	10	3.4	201	14	US-10-206-907-608	Sequence 608, App	646	9	3.1	48	10	US-10-282-122A-67640	Sequence 67640, A
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575	10	3.4	201	14	US-10-183-009-608	Sequence 608, App	648	8	2.8	48	10	US-09-948-783-141	Sequence 141, App
576	10	3.4	201	14	US-10-187-755-608	Sequence 608, App	649	8	2.8	48	12	US-10-616-263-239	Sequence 239, App
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582	10	3.4	201	14	US-10-196-747-608	Sequence 608, App	655	8	2.8	90	14	US-10-188-246-8	Sequence 8, Appli
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585	10	3.4	201	14	US-10-173-691-608	Sequence 608, App	658	8	2.8	103	14	US-10-188-246-4	Sequence 4, Appli
586	10	3.4	201	14	US-10-173-694-608	Sequence 608, App	659	8	2.8	107	8	US-08-927-929-53	Sequence 53, Appli
587	10	3.4	201	14	US-10-173-698-608	Sequence 608, App	660	8	2.8	107	10	US-09-894-159-59	Sequence 59, Appli
588	10	3.4	201	14	US-10-173-699-608	Sequence 608, App	661	8	2.8	107	10	US-09-894-159-60	Sequence 60, Appli
589	10	3.4	201	14	US-10-173-707-608	Sequence 608, App	662	8	2.8	107	12	US-10-170-385-481	Sequence 481, App
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591	10	3.4	201	14	US-10-174-583-608	Sequence 608, App	664	8	2.8	107	15	US-10-440-464-58	Sequence 58, Appli
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593	10	3.4	201	14	US-10-174-589-608	Sequence 608, App	666	8	2.8	131	12	US-10-286-115-1327	Sequence 1327, Ap
594	10	3.4	201	14	US-10-174-591-608	Sequence 608, App	667	8	2.8	138	14	US-10-106-698-6719	Sequence 6719, Ap
595	10	3.4	201	14	US-10-175-736-608	Sequence 608, App	668	8	2.8	153	16	US-10-437-963-126330	Sequence 126330, App
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597	10	3.4	201	14	US-10-175-744-608	Sequence 608, App	670	8	2.8	224	12	US-10-425-114-48788	Sequence 48788, A
598	10	3.4	201	14	US-10-175-745-608	Sequence 608, App	671	8	2.8	224	15	US-10-767-701-41721	Sequence 41721, A
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675	8	2.8	461	14	US-10-410-432-10	Sequence 10,	748	7	2.4	236	16	US-10-126-022-347	Sequence 347, App
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677	8	2.8	472	10	US-09-828-173-7	Sequence 7, Appli	750	7	2.4	247	16	US-10-767-701-46076	Sequence 46076, A
678	8	2.8	472	14	US-10-410-433-7	Sequence 7, Appli	751	7	2.4	249	16	US-10-437-963-154022	Sequence 154022, A
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681	8	2.8	475	14	US-10-410-433-6	Sequence 6, Appli	754	7	2.4	266	12	US-10-425-114-53809	Sequence 53809, A
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687	7	2.4	33	12	US-10-164-861-559	Sequence 559, App	760	7	2.4	283	16	US-10-437-963-103793	Sequence 103793, A
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691	7	2.4	60	10	US-09-984-271-176	Sequence 176, App	764	7	2.4	302	10	US-09-834-597-348	Sequence 348, App
692	7	2.4	60	12	US-09-984-276-176	Sequence 176, App	765	7	2.4	302	15	US-10-277-216-348	Sequence 348, App
693	7	2.4	68	16	US-10-437-963-197340	Sequence 197340,	766	7	2.4	302	16	US-10-126-022-348	Sequence 348, App
694	7	2.4	70	16	US-10-437-963-184480	Sequence 184480,	767	7	2.4	310	12	US-10-425-114-47852	Sequence 47852, A
695	7	2.4	79	16	US-10-437-963-148042	Sequence 148042,	768	7	2.4	320	14	US-10-156-761-9631	Sequence 9631, Ap
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697	7	2.4	90	16	US-10-767-701-40984	Sequence 23956,	770	7	2.4	331	14	US-10-278-946-18	Sequence 18, Appli
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703	7	2.4	107	8	US-08-927-939-57	Sequence 24, Appli	776	7	2.4	360	16	US-10-437-963-105069	Sequence 105069, A
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706	7	2.4	107	10	US-09-894-159-56	Sequence 15, Appli	779	7	2.4	366	16	US-10-437-963-177515	Sequence 177515, A
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739	7	2.4	218	14	US-10-339-740-204	Sequence 204, App	812	7	2.4	564	16	US-10-408-765A-168	Sequence 168, App
740	7	2.4	222	12	US-10-424-599-242628	Sequence 242628,	813	7	2.4	564	16	US-10-697-894-53	Sequence 53, Appli
741	7	2.4	229	12	US-09-758-759-153	Sequence 153, App	814	7	2.4	570	15	US-10-108-260A-4351	Sequence 4351, Ap
742	7	2.4	233	12	US-10-424-599-195297	Sequence 195297,	815	7	2.4	579	10	US-09-890-688-72	Sequence 72, Appli
743	7	2.4	235	10	US-09-834-597-349	Sequence 349, App	816	7	2.4	582	12	US-10-424-599-251471	Sequence 251471, A
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820	7	2.4	16	US-10-437-963-153960	Sequence 153960,	893	7	2.4	813	12	US-10-187-740-466	Sequence 466, App
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822	7	2.4	634	US-10-697-894-51	Sequence 51, Appl	895	7	2.4	813	12	US-10-194-363-466	Sequence 466, App
823	7	2.4	635	US-10-241-220-85	Sequence 85, Appl	896	7	2.4	813	12	US-10-194-460-466	Sequence 466, App
824	7	2.4	642	US-10-335-977-5288	Sequence 5288, Ap	897	7	2.4	813	12	US-10-194-463-466	Sequence 466, App
825	7	2.4	644	US-10-369-493-15638	Sequence 15638, A	898	7	2.4	813	12	US-10-194-484-466	Sequence 466, App
826	7	2.4	644	US-10-369-493-16013	Sequence 16013, A	899	7	2.4	813	12	US-10-195-884-466	Sequence 466, App
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829	7	2.4	684	US-10-437-963-142023	Sequence 142023,	902	7	2.4	813	12	US-10-196-755-466	Sequence 466, App
830	7	2.4	686	US-10-343-251A-4	Sequence 4, Appli	903	7	2.4	813	12	US-10-196-757-466	Sequence 466, App
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832	7	2.4	708	US-10-437-963-111967	Sequence 111967,	905	7	2.4	813	12	US-10-197-710-466	Sequence 466, App
833	7	2.4	717	US-10-437-963-140742	Sequence 140742,	906	7	2.4	813	12	US-10-198-758-466	Sequence 466, App
834	7	2.4	725	US-10-369-493-2004	Sequence 2004, Ap	907	7	2.4	813	12	US-10-198-766-466	Sequence 466, App
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836	7	2.4	732	US-10-107-782-80	Sequence 80, Appl	909	7	2.4	813	12	US-10-199-309-466	Sequence 466, App
837	7	2.4	733	US-10-425-114-68372	Sequence 68372, A	910	7	2.4	813	12	US-10-199-313-466	Sequence 466, App
838	7	2.4	746	US-10-670-184-4	Sequence 4, Appli	911	7	2.4	813	12	US-10-199-456-466	Sequence 466, App
839	7	2.4	756	US-10-282-122A-67072	Sequence 67072, A	912	7	2.4	813	12	US-10-201-329-466	Sequence 466, App
840	7	2.4	759	US-10-099-285-86	Sequence 86, Appl	913	7	2.4	813	12	US-10-202-412-466	Sequence 466, App
841	7	2.4	769	US-10-104-047-2846	Sequence 2846, Ap	914	7	2.4	813	12	US-10-206-919-466	Sequence 466, App
842	7	2.4	786	US-10-698-096-19	Sequence 19, Appl	915	7	2.4	813	12	US-10-206-922-466	Sequence 466, App
843	7	2.4	787	US-10-363-937-16	Sequence 16, Appl	916	7	2.4	813	12	US-10-206-924-466	Sequence 466, App
844	7	2.4	787	US-10-452-002A-54	Sequence 54, Appl	917	7	2.4	813	12	US-10-206-928-466	Sequence 466, App
845	7	2.4	787	US-10-670-184-5	Sequence 5, Appli	918	7	2.4	813	12	US-10-207-914-466	Sequence 466, App
846	7	2.4	787	US-10-698-096-25	Sequence 25, Appl	919	7	2.4	813	12	US-10-207-921-466	Sequence 466, App
847	7	2.4	787	US-10-473-687-2	Sequence 2, Appli	920	7	2.4	813	12	US-10-207-922-466	Sequence 466, App
848	7	2.4	787	US-10-473-687-7	Sequence 7, Appli	921	7	2.4	813	12	US-10-208-027-466	Sequence 466, App
849	7	2.4	788	US-10-156-761-14497	Sequence 14497, A	922	7	2.4	813	12	US-10-174-570-466	Sequence 466, App
850	7	2.4	788	US-10-698-096-27	Sequence 27, Appl	923	7	2.4	813	12	US-10-183-005-466	Sequence 466, App
851	7	2.4	799	US-09-850-351A-6	Sequence 6, Appli	924	7	2.4	813	13	US-10-052-586-466	Sequence 466, App
852	7	2.4	799	US-10-099-285-80	Sequence 80, Appl	925	7	2.4	813	13	US-10-174-590-466	Sequence 466, App
853	7	2.4	799	US-10-099-285-82	Sequence 82, Appl	926	7	2.4	813	13	US-10-176-758-466	Sequence 466, App
854	7	2.4	799	US-10-099-285-84	Sequence 84, Appl	927	7	2.4	813	14	US-10-176-737-466	Sequence 466, App
855	7	2.4	799	US-10-099-285-90	Sequence 90, Appl	928	7	2.4	813	14	US-10-173-706-466	Sequence 466, App
856	7	2.4	799	US-10-099-285-92	Sequence 92, Appl	929	7	2.4	813	14	US-10-175-738-466	Sequence 466, App
857	7	2.4	799	US-10-099-285-94	Sequence 94, Appl	930	7	2.4	813	14	US-10-175-752-466	Sequence 466, App
858	7	2.4	799	US-10-099-285-96	Sequence 96, Appl	931	7	2.4	813	14	US-10-176-482-466	Sequence 466, App
859	7	2.4	799	US-10-099-285-98	Sequence 98, Appl	932	7	2.4	813	14	US-10-176-757-466	Sequence 466, App
860	7	2.4	799	US-10-099-285-100	Sequence 100, App	933	7	2.4	813	14	US-10-176-913-466	Sequence 466, App
861	7	2.4	799	US-10-099-285-100	Sequence 100, App	934	7	2.4	813	14	US-10-180-552-466	Sequence 466, App
862	7	2.4	799	US-10-698-096-6	Sequence 6, Appli	935	7	2.4	813	14	US-10-180-557-466	Sequence 466, App
863	7	2.4	799	US-10-473-687-5	Sequence 5, Appli	936	7	2.4	813	14	US-10-173-700-466	Sequence 466, App
864	7	2.4	799	US-09-850-351A-4	Sequence 4, Appli	937	7	2.4	813	14	US-10-174-572-466	Sequence 466, App
865	7	2.4	799	US-10-099-285-102	Sequence 102, App	938	7	2.4	813	14	US-10-174-579-466	Sequence 466, App
866	7	2.4	799	US-10-452-002A-2	Sequence 2, Appli	939	7	2.4	813	14	US-10-174-582-466	Sequence 466, App
867	7	2.4	799	US-10-698-096-4	Sequence 4, Appli	940	7	2.4	813	14	US-10-174-588-466	Sequence 466, App
868	7	2.4	799	US-10-698-096-8	Sequence 8, Appli	941	7	2.4	813	14	US-10-175-739-466	Sequence 466, App
869	7	2.4	801	US-10-282-122A-70493	Sequence 70493, A	942	7	2.4	813	14	US-10-175-740-466	Sequence 466, App
870	7	2.4	812	US-09-834-597-363	Sequence 363, App	943	7	2.4	813	14	US-10-175-743-466	Sequence 466, App
871	7	2.4	812	US-10-399-645-3	Sequence 3, Appli	944	7	2.4	813	14	US-10-176-488-466	Sequence 466, App
872	7	2.4	812	US-10-177-308-4	Sequence 4, Appli	945	7	2.4	813	14	US-10-176-492-466	Sequence 466, App
873	7	2.4	812	US-10-028-248A-79	Sequence 79, Appl	946	7	2.4	813	14	US-10-176-747-466	Sequence 466, App
874	7	2.4	812	US-10-271-216-363	Sequence 363, App	947	7	2.4	813	14	US-10-176-750-466	Sequence 466, App
875	7	2.4	812	US-10-107-782-79	Sequence 79, Appl	948	7	2.4	813	14	US-10-176-985-466	Sequence 466, App
876	7	2.4	812	US-10-126-022-363	Sequence 363, App	949	7	2.4	813	14	US-10-176-987-466	Sequence 466, App
877	7	2.4	812	US-10-343-251A-21	Sequence 21, Appl	950	7	2.4	813	14	US-10-176-992-466	Sequence 466, App
878	7	2.4	813	US-10-206-915-466	Sequence 466, App	951	7	2.4	813	14	US-10-176-993-466	Sequence 466, App
879	7	2.4	813	US-10-199-670-466	Sequence 466, App	952	7	2.4	813	14	US-10-184-658-466	Sequence 466, App
880	7	2.4	813	US-10-201-858-466	Sequence 466, App	953	7	2.4	813	14	US-10-176-991-466	Sequence 466, App
881	7	2.4	813	US-10-205-890-466	Sequence 466, App	954	7	2.4	813	14	US-10-173-695-466	Sequence 466, App
882	7	2.4	813	US-10-208-024-466	Sequence 466, App	955	7	2.4	813	14	US-10-173-697-466	Sequence 466, App
883	7	2.4	813	US-10-208-024-466	Sequence 466, App	956	7	2.4	813	14	US-10-173-705-466	Sequence 466, App
884	7	2.4	813	US-10-174-581-466	Sequence 466, App	957	7	2.4	813	14	US-10-174-576-466	Sequence 466, App
885	7	2.4	813	US-10-176-483-466	Sequence 466, App	958	7	2.4	813	14	US-10-174-585-466	Sequence 466, App
886	7	2.4	813	US-10-176-749-466	Sequence 466, App	959	7	2.4	813	14	US-10-174-586-466	Sequence 466, App
887	7	2.4	813	US-10-176-914-466	Sequence 466, App	960	7	2.4	813	14	US-10-175-747-466	Sequence 466, App
888	7	2.4	813	US-10-176-915-466	Sequence 466, App	961	7	2.4	813	14	US-10-176-481-466	Sequence 466, App
889	7	2.4	813	US-10-176-484-466	Sequence 466, App	962	7	2.4	813	14	US-10-176-485-466	Sequence 466, App
890	7	2.4	813	US-10-180-550-466	Sequence 466, App	963	7	2.4	813	14	US-10-176-487-466	Sequence 466, App
891	7	2.4	813	US-10-183-014-466	Sequence 466, App	964	7	2.4	813	14	US-10-176-493-466	Sequence 466, App

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965 7 2.4 813 14 US-10-176-756-466 Sequence 466, App
 966 7 2.4 813 14 US-10-176-911-466 Sequence 466, App
 967 7 2.4 813 14 US-10-176-919-466 Sequence 466, App
 968 7 2.4 813 14 US-10-176-925-466 Sequence 466, App
 969 7 2.4 813 14 US-10-176-978-466 Sequence 466, App
 970 7 2.4 813 14 US-10-179-510-466 Sequence 466, App
 971 7 2.4 813 14 US-10-180-543-466 Sequence 466, App
 972 7 2.4 813 14 US-10-180-544-466 Sequence 466, App
 973 7 2.4 813 14 US-10-180-546-466 Sequence 466, App
 974 7 2.4 813 14 US-10-180-547-466 Sequence 466, App
 975 7 2.4 813 14 US-10-180-549-466 Sequence 466, App
 976 7 2.4 813 14 US-10-180-555-466 Sequence 466, App
 977 7 2.4 813 14 US-10-180-559-466 Sequence 466, App
 978 7 2.4 813 14 US-10-181-000-466 Sequence 466, App
 979 7 2.4 813 14 US-10-183-010-466 Sequence 466, App
 980 7 2.4 813 14 US-10-183-012-466 Sequence 466, App
 981 7 2.4 813 14 US-10-184-614-466 Sequence 466, App
 982 7 2.4 813 14 US-10-184-623-466 Sequence 466, App
 983 7 2.4 813 14 US-10-184-635-466 Sequence 466, App
 984 7 2.4 813 14 US-10-184-637-466 Sequence 466, App
 985 7 2.4 813 14 US-10-184-646-466 Sequence 466, App
 986 7 2.4 813 14 US-10-184-647-466 Sequence 466, App
 987 7 2.4 813 14 US-10-184-652-466 Sequence 466, App
 988 7 2.4 813 14 US-10-187-594-466 Sequence 466, App
 989 7 2.4 813 14 US-10-187-596-466 Sequence 466, App
 990 7 2.4 813 14 US-10-187-745-466 Sequence 466, App
 991 7 2.4 813 14 US-10-187-885-466 Sequence 466, App
 992 7 2.4 813 14 US-10-187-886-466 Sequence 466, App
 993 7 2.4 813 14 US-10-199-464-466 Sequence 466, App
 994 7 2.4 813 14 US-10-196-756-466 Sequence 466, App
 995 7 2.4 813 14 US-10-176-751-466 Sequence 466, App
 996 7 2.4 813 14 US-10-176-760-466 Sequence 466, App
 997 7 2.4 813 14 US-10-176-990-466 Sequence 466, App
 998 7 2.4 813 14 US-10-180-541-466 Sequence 466, App
 999 7 2.4 813 14 US-10-180-542-466 Sequence 466, App
 1000 7 2.4 813 14 US-10-180-548-466 Sequence 466, App

ALIGNMENTS

RESULT 1
 US-09-965-529-18
 ; Sequence 18, Application US/09965529
 ; Publication No. US20020182671A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: YUE, Henry
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil
 ; APPLICANT: AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: LU, Dyung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731 USA
 ; CURRENT APPLICATION NUMBER: US/09/965,529
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
 ; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 18
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020182671A1 1562471CD1
 ; US-09-965-529-18
 Query Match 57.2%; Score 166; DB 9; Length 290;

Best Local Similarity 99.6%; Pred. No. 6.5e-151;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPLLTYLLFWLSGYSIATQITPTTVNGLERSLTVQCYVRSWETYLKWCRCGAIWR 60
 Db 1 MPLLTYLLFWLSGYSIATQITPTTVNGLERSLTVQCYVRSWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVITDPAPVTOEETSSPTLTGHHLNRRHKLKLSVLLPLIFITXILLVVAASLLAWRM 180
 Db 121 VQVITDPAPVTOEETSSPTLTGHHLNRRHKLKLSVLLPLIFITXILLVVAASLLAWRM 180
 QY 181 MKYQKAGMSPEQVLOPLEGDLQVADLTLOLACTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAGMSPEQVLOPLEGDLQVADLTLOLACTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEQETPCNMG 267
 Db 241 SLPKEDISYASLTGAEDEQETPCNMG 267
 RESULT 2
 US-09-969-680A-18
 ; Sequence 18, Application US/09969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969,680A
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US00/22315
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149,641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164,203
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 18
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 1562471CD1
 ; US-09-969-680A-18
 Query Match 57.2%; Score 166; DB 10; Length 290;
 Best Local Similarity 99.6%; Pred. No. 6.5e-151;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPLLTYLLFWLSGYSIATQITPTTVNGLERSLTVQCYVRSWETYLKWCRCGAIWR 60
 Db 1 MPLLTYLLFWLSGYSIATQITPTTVNGLERSLTVQCYVRSWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVITDPAPVTOEETSSPTLTGHHLNRRHKLKLSVLLPLIFITXILLVVAASLLAWRM 180
 Db 121 VQVITDPAPVTOEETSSPTLTGHHLNRRHKLKLSVLLPLIFITXILLVVAASLLAWRM 180
 QY 181 MKYQKAGMSPEQVLOPLEGDLQVADLTLOLACTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAGMSPEQVLOPLEGDLQVADLTLOLACTSPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQKAAAGMSPQVLPQLEGLDLCYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267

RESULT 3
US-10-219-535-40
; Sequence 40, Application US/10219535
; Publication No. US20040044119A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C60
; CURRENT APPLICATION NUMBER: US/10/219,535
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-535-40

Query Match 57.2%; Score 166; DB 12; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSQSEQVKKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLDVT 120
Db 61 DCKILVKTSQSEQVKKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLDVT 120

QY 121 VQVTTIDPAPVQTESSPTLTGHLDNRHKLKLSVLLPLFTTXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVQTESSPTLTGHLDNRHKLKLSVLLPLFTTXLLLLVAASLLAWRM 180

QY 181 MKYQKAAAGMSPQVLPQLEGLDLCYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQKAAAGMSPQVLPQLEGLDLCYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267

RESULT 4
US-10-232-230-40
; Sequence 40, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C03
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-40

Query Match 57.2%; Score 166; DB 12; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSQSEQVKKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLDVT 120
Db 61 DCKILVKTSQSEQVKKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLDVT 120

QY 121 VQVTTIDPAPVQTESSPTLTGHLDNRHKLKLSVLLPLFTTXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVQTESSPTLTGHLDNRHKLKLSVLLPLFTTXLLLLVAASLLAWRM 180

QY 181 MKYQKAAAGMSPEQVLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAAAGMSPEQVLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEQPTCYNMG 267

RESULT 5

US-10-232-224-40
 ; Sequence 40, Application US/10232224
 ; Publication No. US20030065147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3530PIC11
 ; CURRENT APPLICATION NUMBER: US/10/232,224
 ; CURRENT FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 40
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-232-224-40

Query Match 57.2%; Score 166; DB 12; Length 290;
 Best Local Similarity 99.6%; Pred. No. 6.5e-151;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPLLTLYLFWLSCYSIATQITPTTVNGLERGLTVCQVYRSGWETYLKWWCRGAIWR 60
 Db 1 MPLLTLYLFWLSCYSIATQITPTTVNGLERGLTVCQVYRSGWETYLKWWCRGAIWR 60
 QY 61 DCKILVKTSGEQVYRSGWETYLKWWCRGAIWR 120
 Db 61 DCKILVKTSGEQVYRSGWETYLKWWCRGAIWR 120
 QY 121 VQVITDPAVPTQETSSPTTIGHLDNRHKLKLVLLPLIFTXILLVLAASLLAWRM 180
 Db 121 VQVITDPAVPTQETSSPTTIGHLDNRHKLKLVLLPLIFTXILLVLAASLLAWRM 180

QY 181 MKYQKAAAGMSPEQVLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAAAGMSPEQVLQPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEQPTCYNMG 267

RESULT 6

US-10-227-884-40
 ; Sequence 40, Application US/10227884
 ; Publication No. US20030027988A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3530PIC79
 ; CURRENT APPLICATION NUMBER: US/10/227,884
 ; CURRENT FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
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 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/085123
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 ; PRIOR APPLICATION NUMBER: 60/085579
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 ; PRIOR APPLICATION NUMBER: 60/089532
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 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089905
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
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; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
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; PRIOR FILING DATE: 1998-11-17
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; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422

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; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
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; PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1999-02-10
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; PRIOR FILING DATE: 1999-04-28
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; PRIOR FILING DATE: 1999-06-22
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; PRIOR FILING DATE: 1999-08-31
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPULLYLLFWLSGYSIATQITGPTVNGLSLTVCVRSQWETYLKWCRCGAIWR 60
|||||

1 100% 100%

Db 1 MPLLTYLLEWLSGYSIATQITGTTVNGLSGLTVQCVYRSGWETYLKWWCRGAIWR 60
QY 61 DCKILVKTSGSEQVVKRDRVSIKONOKRFTFTVMTEDLMKTDADTYWCGIEKTDNLGVT 120
Db 61 DCKILVKTSGSEQVVKRDRVSIKONOKRFTFTVMTEDLMKTDADTYWCGIEKTDNLGVT 120
QY 121 VQVITDPAPVTQETSSPTTIGHLONRHKLLKLSVLLPLIFITXLLLLVAASLLAWRM 180
Db 121 VQVITDPAPVTQETSSPTTIGHLONRHKLLKLSVLLPLIFITXLLLLVAASLLAWRM 180
QY 181 MKYQKAAAGMPEQVQLQLEGDLVADLTQLAGTSRPRKATTKLSSAQVQVVEYYTMA 240
Db 181 MKYQKAAAGMPEQVQLQLEGDLVADLTQLAGTSRPRKATTKLSSAQVQVVEYYTMA 240
QY 241 SLPKEDISYASLTIGAEDQETFCNMG 267
Db 241 SLPKEDISYASLTIGAEDQETFCNMG 267

RESULT 7
US-10-230-163-40
; Sequence 40, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/113,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
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; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
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; PRIOR APPLICATION NUMBER: 60/097986
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; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
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; PRIOR APPLICATION NUMBER: 60/149638
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495

; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATGTTVNGLSLTVQCVYRSGWETYLKWCRCALWR 60
DB 1 MPLLTLVLLFWLSGYSIATGTTVNGLSLTVQCVYRSGWETYLKWCRCALWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
QY 121 VQVTIDPAPVTQEBTSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLXLLVAASLLAWRM 180
DB 121 VQVTIDPAPVTQEBTSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLXLLVAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLPQLEGLDLCVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQQAAGMSPEQVLPQLEGLDLCVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDQEPTYCNMG 267
DB 241 SLPKEDISYASLTGAEDQEPTYCNMG 267

RESULT 8
US-10-230-338-40
; Sequence 40, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-631-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVTDIPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTDIPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQKKAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKKAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTYCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTYCNMG 267

RESULT 9
US-10-218-631-40
; Sequence 40, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40

; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVTDIPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTDIPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQKKAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKKAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTYCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTYCNMG 267

RESULT 10
US-10-230-414-40
; Sequence 40, Application US/10230414
; Publication No. US2003005048A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 41
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; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-40

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAPVTQETSSPFLTGHHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
DB 121 VQVITDPAPVTQETSSPFLTGHHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYV 240
DB 181 MKYQQAAGMSPQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTGAEDEQPTTCNM 267
DB 241 SLPKEDISYASLTGAEDEQPTTCNM 267

RESULT 11
US-10-216-159A-40
; Sequence 40, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-40

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAPVTQETSSPFLTGHHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
DB 121 VQVITDPAPVTQETSSPFLTGHHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYV 240
DB 181 MKYQQAAGMSPQVLPQLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTGAEDEQPTTCNM 267
DB 241 SLPKEDISYASLTGAEDEQPTTCNM 267

RESULT 12
US-10-218-849-40
; Sequence 40, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-40

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTDPAVPTQETSSPTTGHHLNDRHKLKLSVLLPFTIXLLVLAASLLAWRM 180
Db 121 VQVTDPAVPTQETSSPTTGHHLNDRHKLKLSVLLPFTIXLLVLAASLLAWRM 180
QY 181 MKYQKAAGNSPEQVQPLEGDLVADLTQLAGTSRKATTKLSSAQVDQVEVYVTMA 240
Db 181 MKYQKAAGNSPEQVQPLEGDLVADLTQLAGTSRKATTKLSSAQVDQVEVYVTMA 240
QY 241 SLPKEDISYASLTGAEQDEPTYCNMG 267
Db 241 SLPKEDISYASLTGAEQDEPTYCNMG 267

RESULT 13
US-10-227-873-40
; Sequence 40, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905

; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Prec.No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTLVLLFWLWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVTSQSEQVEKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
DB 61 DCKILVTSQSEQVEKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVITDPAPVTOEBTSSPTLTGHLDNRHKLKLSVLLPLFIETIXILLVVAASLLAWRM 180
DB 121 VQVITDPAPVTOEBTSSPTLTGHLDNRHKLKLSVLLPLFIETIXILLVVAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLOPLEGDLICYADITLQOLACTSPRKATTKLSSAQVDOVEVEYVTMA 240
DB 181 MKYQOKAAGMSPEQVLOPLEGDLICYADITLQOLACTSPRKATTKLSSAQVDOVEVEYVTMA 240
QY 241 SLPKEDISYASLTIGABDQEBTYCNMG 267
DB 241 SLPKEDISYASLTIGABDQEBTYCNMG 267
RESULT 14
US-10-227-883-40
; Sequence 40, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13

/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/086392
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/089532
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089538
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089905
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090472
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090691
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090695
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/095302
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/095318
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/095916
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/096146
/ PRIOR FILING DATE: 1998-08-11
/ PRIOR APPLICATION NUMBER: 60/096791
/ PRIOR FILING DATE: 1998-08-17
/ PRIOR APPLICATION NUMBER: 60/097986
/ PRIOR FILING DATE: 1998-08-26
/ PRIOR APPLICATION NUMBER: 60/098544
/ PRIOR FILING DATE: 1998-08-31
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; PRIOR APPLICATION NUMBER: 60/169835

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Best Local Similarity 99.6%; Pred. No. 6.5e-151;
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Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQVVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
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QY 181 MKYQOKAAGMSPEQVLOPLEGDLQVADLTLOLAGTSRKATTKLSSAQVDQVEVEYV 240
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; Sequence 40, Application US/10219076
; Publication No. US20030078379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P35301C62
; CURRENT APPLICATION NUMBER: US/10/219,076
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
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; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-219-076-40
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Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQVVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTDIPAPVTOBETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VQVTDIPAPVTOBETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLOPLEGDLQVADLTLOLAGTSRKATTKLSSAQVDQVEVEYV 240
Db 181 MKYQOKAAGMSPEQVLOPLEGDLQVADLTLOLAGTSRKATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267

Search completed: September 16, 2004, 13:08:32
Job time : 142 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:49:37 ; Search time 41 Seconds
(without alignments)

680.379 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290

Sequence: 1 MPILTYLLFLWLSGYSIAT.....SXLPGRGPPEPTYSISRPP 290

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR.78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.8	107	2 B38290	GRO-gamma precursor
2	8	2.8	107	2 JH0281	macrophage inflam
3	8	2.8	475	2 A12439	hypothetical prote
4	8	2.8	600	2 C90171	RNase L inhibitor
5	7	2.4	92	2 C30552	macrophage inflam
6	7	2.4	99	2 D90259	hypothetical prote
7	7	2.4	107	2 A28414	melanoma growth-st
8	7	2.4	109	2 I49011	gene Ubely protein
9	7	2.4	109	2 I63169	gene Ubely protein
10	7	2.4	111	2 B70401	hypothetical prote
11	7	2.4	120	2 A87594	bleomycin resistan
12	7	2.4	120	2 C81087	hypothetical prote
13	7	2.4	145	2 D82105	conserved hypothet
14	7	2.4	164	2 B44827	FMRFamide-like pep
15	7	2.4	167	2 C86241	protein T16B5.9 [i
16	7	2.4	171	2 H83233	conserved hypothet
17	7	2.4	175	2 T21297	FMRFamide-like neu
18	7	2.4	185	2 D81229	ribosome recycling
19	7	2.4	187	2 G72748	hypothetical prote
20	7	2.4	194	2 D73357	hypothetical prote
21	7	2.4	210	2 S76316	hypothetical prote
22	7	2.4	218	2 T33545	hypothetical prote
23	7	2.4	255	2 F49962	amino acid ABC tra
24	7	2.4	257	2 B75099	hypothetical prote
25	7	2.4	258	2 G89968	extracellular ente
26	7	2.4	268	1 CDFM18	chlorophyll a/b-bi
27	7	2.4	284	2 A75422	acetyl-CoA carboxy
28	7	2.4	284	2 AH3570	nickel transport s
29	7	2.4	287	2 A84041	sulfate ABC transp

30	7	2.4	289	2 S19998	hypothetical prote
31	7	2.4	299	2 F83301	conserved hypothet
32	7	2.4	309	2 H89832	hypothetical prote
33	7	2.4	311	2 A72487	hypothetical prote
34	7	2.4	319	2 G86832	hypothetical prote
35	7	2.4	324	2 B24582	H-2 class I histoc
36	7	2.4	327	2 D75196	hypothetical prote
37	7	2.4	331	2 F89771	lipoprotein [impor
38	7	2.4	334	2 A24582	MHC class I histoc
39	7	2.4	335	1 SAVLHH	large surface anti
40	7	2.4	338	2 F95880	probable thur, reg
41	7	2.4	340	2 A45883	MHC class I histoc
42	7	2.4	357	2 G70869	probable uroporph
43	7	2.4	361	2 I37421	glutaminyl-peptid
44	7	2.4	362	2 F75379	S-adenosylmethioni
45	7	2.4	372	2 S60207	fomF protein - Str
46	7	2.4	380	2 A50107	hypothetical prote
47	7	2.4	397	2 B72211	glutamate N-acetyl
48	7	2.4	400	2 S32804	beta-3-adrenergic
49	7	2.4	400	2 A41679	beta-3-adrenergic
50	7	2.4	400	2 A53281	beta-3-adrenergic
51	7	2.4	416	2 A70393	hypothetical prote
52	7	2.4	417	2 F70681	hypothetical prote
53	7	2.4	422	2 G84059	hypothetical prote
54	7	2.4	442	2 S19712	ubiquitin-protein
55	7	2.4	461	2 T38698	nocl protein - fis
56	7	2.4	508	2 S54264	glycoprotein GC -
57	7	2.4	513	2 E83069	catalase PA4613 [i
58	7	2.4	519	2 E72021	60K chaperonin, pr
59	7	2.4	519	2 H86602	heat shock protein
60	7	2.4	521	1 VGBEBB	glycoprotein gIII
61	7	2.4	533	2 F75124	abc transporter in
62	7	2.4	533	2 A73449	mannitol transport
63	7	2.4	538	2 D82180	probable sensor ki
64	7	2.4	554	2 S46346	gag polyprotein -
65	7	2.4	561	1 S53447	aspartate-ammonia
66	7	2.4	561	1 AHRNC	asparagine synthas
67	7	2.4	587	2 E85429	hypothetical prote
68	7	2.4	598	2 D69292	aldehyde ferredoxi
69	7	2.4	599	2 G83941	ABC transporter (A
70	7	2.4	641	2 JCS648	terminal protein p
71	7	2.4	642	2 D71909	ferrous iron trans
72	7	2.4	642	2 G84605	iron(II) transport
73	7	2.4	643	2 T27429	hypothetical prote
74	7	2.4	716	1 W2BEE6	77.8K DNA helicase
75	7	2.4	725	2 A41258	a-aggglutinin core
76	7	2.4	751	2 T42597	DNA helicase/prima
77	7	2.4	822	2 T33163	hypothetical prote
78	7	2.4	900	2 A95340	cation transport p
79	7	2.4	911	1 B3HU	band 3 anion trans
80	7	2.4	968	2 A37867	transcription fact
81	7	2.4	971	2 A35697	ice nucleation pro
82	7	2.4	989	2 AE3045	hypothetical prote
83	7	2.4	1009	2 G98240	probable large ATP
84	7	2.4	1010	2 T36383	hypothetical prote
85	7	2.4	1013	2 T48422	hypothetical prote
86	7	2.4	1047	1 OYHUBR	natruetic peptid
87	7	2.4	1065	2 S19482	hypothetical prote
88	7	2.4	1067	2 D75625	probable extracell
89	7	2.4	1089	2 E82987	hypothetical prote
90	7	2.4	1099	2 A55405	adenylate cyclase
91	7	2.4	1103	2 JC4114	Ca2+-transporting
92	7	2.4	1184	2 G76600	hypothetical prote
93	7	2.4	1242	2 T39453	probable mna stab
94	7	2.4	1268	2 T50252	probable transcrip
95	7	2.4	1288	2 JEO363	mitogen-activated
96	7	2.4	1400	1 I38185	protein-tyrosine k
97	7	2.4	2491	1 A28372	insulin-like growt
98	7	2.4	4717	1 T41581	hypothetical coile
99	6	2.1	21	2 S03979	tetosterone 15alp
100	6	2.1	36	2 B27633	Ig lambda-2 chain
101	6	2.1	36	2 S78239	ycf32 protein - Od
102	6	2.1	47	2 S42126	hypothetical prote

103	6	2.1	48	2	A30504	Ig gamma heavy chain	176	6	2.1	137	2	S31585	Ig heavy chain V r
104	6	2.1	50	2	S05487	alpha-amylase (EC	177	6	2.1	137	2	AD1179	B. subtilis Yrkr p
105	6	2.1	52	2	G81536	hypothetical prote	178	6	2.1	137	2	AD1536	B. subtilis Yrkr p
106	6	2.1	54	2	U00155	spore protein gamm	179	6	2.1	137	2	A69127	hypothetical prote
107	6	2.1	55	2	S29146	superoxide dismuta	180	6	2.1	138	2	AC2255	two-component resp
108	6	2.1	57	2	S09493	Ig heavy chain pre	181	6	2.1	139	2	AC1287	Ig heavy chain pre
109	6	2.1	58	2	T13185	hypothetical prote	182	6	2.1	139	2	S31586	Ig heavy chain V r
110	6	2.1	59	2	S35177	cytochrome P450 (c	183	6	2.1	139	2	S31696	Ig heavy chain V r
111	6	2.1	64	1	N5R5L	neurotoxin V - EGY	184	6	2.1	139	2	B75307	hypothetical prote
112	6	2.1	64	1	N5R5M	neurotoxin V - sco	185	6	2.1	139	2	B75307	hypothetical prote
113	6	2.1	65	2	AB3394	hypothetical cytos	186	6	2.1	140	2	S78052	Ig heavy chain pre
114	6	2.1	66	2	D72607	hypothetical prote	187	6	2.1	140	2	A49045	Ig heavy chain V r
115	6	2.1	70	1	RGBPHK	regulatory protein	188	6	2.1	140	2	A24770	hypothetical hybri
116	6	2.1	76	2	T51499	hypothetical prote	189	6	2.1	140	2	I37782	Ig variable region
117	6	2.1	77	2	A30522	Ig gamma-3 heavy c	190	6	2.1	140	2	H72710	hypothetical prote
118	6	2.1	79	2	T63681	proteinase inhibit	191	6	2.1	141	2	T14936	hypothetical prote
119	6	2.1	79	2	B95867	conserved hypotet	192	6	2.1	141	2	T09251	embryonic abundant
120	6	2.1	79	2	AG1062	bacteriophage gene	193	6	2.1	142	2	H71061	hypothetical prote
121	6	2.1	80	2	AB1932	hypothetical prote	194	6	2.1	142	2	H86046	hypothetical prote
122	6	2.1	81	2	T31199	hypothetical prote	195	6	2.1	142	2	D91200	hypothetical prote
123	6	2.1	82	2	JC7897	defensin 1 precurs	196	6	2.1	143	2	B41287	Ig heavy chain pre
124	6	2.1	84	2	T03084	hypothetical prote	197	6	2.1	145	2	S78055	Ig heavy chain pre
125	6	2.1	86	1	RH1D2S	gonadoliberin II p	198	6	2.1	146	2	S09710	Ig heavy chain V r
126	6	2.1	86	2	S72726	lipB1 protein - My	199	6	2.1	147	2	S35519	Ig heavy chain V r
127	6	2.1	88	2	AG1356	hypothetical prote	200	6	2.1	152	2	S08350	superoxide dismuta
128	6	2.1	90	2	G75317	hypothetical prote	201	6	2.1	152	2	S55402	hypothetical prote
129	6	2.1	91	2	C82657	hypothetical prote	202	6	2.1	153	2	S89092	hypothetical prote
130	6	2.1	92	2	S77498	ribosomal protein	203	6	2.1	154	2	H81175	hypothetical prote
131	6	2.1	96	2	S06689	hypothetical prote	204	6	2.1	155	2	S31512	Ig heavy chain - h
132	6	2.1	98	2	PH1145	Ig heavy chain V r	205	6	2.1	155	2	S31511	Ig heavy chain - h
133	6	2.1	98	2	AB2100	hypothetical prote	206	6	2.1	156	2	C81868	hypothetical prote
134	6	2.1	100	2	AB1035	probable phage tai	207	6	2.1	156	2	C64300	hypothetical prote
135	6	2.1	101	2	C83047	conserved hypotet	208	6	2.1	156	2	D81722	hypothetical prote
136	6	2.1	103	1	ZGBPS1	gene G protein - p	209	6	2.1	156	2	AC0540	probable fibrial
137	6	2.1	103	2	T20883	hypothetical prote	210	6	2.1	156	2	D81722	probable fibrial
138	6	2.1	103	2	A59031	ARS component B 81	211	6	2.1	157	2	T02034	early light-induce
139	6	2.1	104	2	F72753	hypothetical prote	212	6	2.1	157	2	T02034	large-conductance
140	6	2.1	106	2	S56222	probable membrane	213	6	2.1	159	2	JQ0136	hypothetical prote
141	6	2.1	108	2	A13250	virA/G regulated p	214	6	2.1	160	2	AD1061	DNA polymerase III
142	6	2.1	109	2	S12338	virH protein - Agr	215	6	2.1	160	2	C70049	flagellar protein
143	6	2.1	109	2	H72653	hypothetical prote	216	6	2.1	162	2	F84424	probable homeodoma
144	6	2.1	110	2	AB1361	Portein gp13 [Bact	217	6	2.1	163	1	YCFC3H	acetylactate synth
145	6	2.1	112	2	S34818	nifW protein - Rho	218	6	2.1	163	2	F83059	acetylactate synth
146	6	2.1	113	2	S69677	probable membrane	219	6	2.1	163	2	S3059	acetylactate synth
147	6	2.1	115	2	H70778	probable acpM prot	220	6	2.1	163	2	B90639	acetylactate synth
148	6	2.1	116	2	B26340	Ig heavy chain pre	221	6	2.1	163	2	B85490	acetylactate synth
149	6	2.1	116	2	S18557	Ig heavy chain V r	222	6	2.1	163	2	A83474	hypothetical prote
150	6	2.1	116	2	G72779	hypothetical prote	223	6	2.1	164	2	D82072	acetylactate synth
151	6	2.1	117	1	ESAD01	early E3 13K Glyco	224	6	2.1	164	2	AB0067	acetylactate synth
152	6	2.1	117	2	E34964	Ig heavy chain pre	225	6	2.1	164	2	AB0517	hypothetical prote
153	6	2.1	118	2	A26340	Ig heavy chain pre	226	6	2.1	164	2	AB0517	hypothetical prote
154	6	2.1	118	2	T31776	hypothetical prote	227	6	2.1	165	2	AD1014	chorismate lyase [
155	6	2.1	118	2	G37857	hypothetical prote	228	6	2.1	165	2	T14781	hypothetical prote
156	6	2.1	120	2	AB1030	probable membrane	229	6	2.1	166	2	H64605	hypothetical prote
157	6	2.1	121	2	H82473	hypothetical prote	230	6	2.1	167	2	AD1978	hypothetical prote
158	6	2.1	124	1	N5RY	pancreatic ribonuc	231	6	2.1	168	2	G59217	hypothetical prote
159	6	2.1	124	2	S31684	Ig heavy chain V r	232	6	2.1	168	2	B98836	conserved hypotet
160	6	2.1	125	2	S09365	Ig kappa chain - m	233	6	2.1	169	1	C84393	hemerythrin homolo
161	6	2.1	127	2	S06347	thyroglobulin - sh	234	6	2.1	170	2	D70621	probable argR prot
162	6	2.1	127	2	F95929	hypothetical membr	235	6	2.1	171	1	OTNCV	cytochrome-c oxida
163	6	2.1	127	2	H87494	cscB protein (impo	236	6	2.1	171	2	B69345	hypothetical prote
164	6	2.1	128	2	T35073	probable phosphori	237	6	2.1	171	2	S19502	hypothetical prote
165	6	2.1	128	2	S73593	hypothetical prote	238	6	2.1	171	2	A47303	FTZ-F1 steroid rec
166	6	2.1	129	2	H83408	hypothetical prote	239	6	2.1	172	2	A70828	hypothetical prote
167	6	2.1	130	2	S22808	pancreatic ribonuc	240	6	2.1	174	2	T28764	hypothetical prote
168	6	2.1	130	2	S31673	Ig heavy chain V r	241	6	2.1	176	2	AD0472	probable fibrial
169	6	2.1	130	2	S62401	interleukin-16 - g	242	6	2.1	176	2	AB0414	hypoxanthine phosph
170	6	2.1	132	2	JH0407	myelin P2 protein	243	6	2.1	178	2	T20317	hypothetical prote
171	6	2.1	132	2	PC4020	hypothetical 132 p	244	6	2.1	182	2	AB2331	50S ribosomal prot
172	6	2.1	133	2	AG9917	hypothetical prote	245	6	2.1	183	2	E82898	conserved hypotet
173	6	2.1	134	2	G72465	hypothetical prote	246	6	2.1	184	2	S31065	type 1 fibrial pr
174	6	2.1	135	2	S78051	Ig heavy chain pre	247	6	2.1	185	2	A82752	hypothetical prote
175	6	2.1	137	2	S31676	Ig heavy chain V r	248	6	2.1	185	2	H50540	hypothetical prote
										186	2	B70595	hypothetical prote

249	6	2.1	187	2	T49222	stellacyanin (ucla	322	6	2.1	231	1	A42985	3-oxoadipate CoA-t
250	6	2.1	187	2	S22331	gene G protein - p	323	6	2.1	231	2	D81441	probable integral
251	6	2.1	187	2	TC4806	core protein G - p	324	6	2.1	231	2	C97313	uncharacterized co
252	6	2.1	187	2	A86363	hypothetical prote	325	6	2.1	232	2	G95044	conserved hypothet
253	6	2.1	187	2	R86478	protein F1504.9 [1	326	6	2.1	232	2	F97914	conserved hypothet
254	6	2.1	188	2	C90808	probable cytochrom	327	6	2.1	233	2	T36385	proline-rich prote
255	6	2.1	188	2	G85667	probable cytochrom	328	6	2.1	234	2	A81871	probable periplasm
256	6	2.1	188	2	F64848	exopolysaccharide	329	6	2.1	235	2	F76974	hypothetical prote
257	6	2.1	188	2	G87544	hypothetical prote	330	6	2.1	235	2	T43009	HMG protein 1.2 -
258	6	2.1	188	2	T48200	hypothetical prote	331	6	2.1	236	2	G95212	MgcC/SapB family p
259	6	2.1	191	2	E84740	hypothetical prote	332	6	2.1	236	2	G98076	Mg(2+) transport A
260	6	2.1	193	2	E75543	peptidylprolyl iso	333	6	2.1	236	2	H1056	probable arylmalon
261	6	2.1	193	2	G97238	uncharacterized me	334	6	2.1	237	2	JQ0061	hypothetical 25K p
262	6	2.1	194	2	S07260	histone H5 - musco	335	6	2.1	237	2	S85009	H+-transporting tw
263	6	2.1	195	2	F96734	probable transcrip	336	6	2.1	238	2	T35088	probable membrane
264	6	2.1	197	2	T10284	hypothetical prote	337	6	2.1	238	2	F89940	conserved hypothet
265	6	2.1	197	2	JC6544	tumor-associated a	338	6	2.1	239	2	F82386	amino acid ABC tra
266	6	2.1	197	2	F70832	probable membrane	339	6	2.1	239	2	H72667	hypothetical prote
267	6	2.1	197	2	E84606	probable Wkry-type	340	6	2.1	239	2	C72778	hypothetical prote
268	6	2.1	198	2	S73275	hypothetical prote	341	6	2.1	239	2	H75195	hypothetical prote
269	6	2.1	198	2	T08910	hypothetical prote	342	6	2.1	239	2	B40710	CD30 ligand - mous
270	6	2.1	201	2	T35017	protocatechuate 3,	343	6	2.1	240	2	UN0407	polyhedrin - Galle
271	6	2.1	201	2	T06229	probable superoxid	344	6	2.1	241	2	B64800	Glutamate/aspartat
272	6	2.1	201	2	T06800	superoxide dismuta	345	6	2.1	241	2	C90715	Glutamate/aspartat
273	6	2.1	201	2	AF2089	hypothetical prote	346	6	2.1	241	2	F85565	Glutamate/aspartat
274	6	2.1	202	1	DSPMC2	superoxide dismuta	347	6	2.1	241	2	AC0583	glutamate/aspartat
275	6	2.1	203	2	A75453	conserved hypothet	348	6	2.1	242	2	A25192	C-reactive protein
276	6	2.1	203	2	AB2285	hypothetical prote	349	6	2.1	242	2	AC0131	probable copper ho
277	6	2.1	204	2	T28939	hypothetical prote	350	6	2.1	243	2	S86734	nicotinamide monon
278	6	2.1	205	2	B84334	hypothetical prote	351	6	2.1	244	1	S37397	regulatory protein
279	6	2.1	206	2	S76522	hypothetical prote	352	6	2.1	244	2	AC3341	pricornin-2 C20-me
280	6	2.1	206	2	E89961	N-acetylmuramoyl-L	353	6	2.1	244	2	A70400	hypothetical prote
281	6	2.1	207	2	E69833	conserved hypothet	354	6	2.1	245	2	C72382	conserved hypothet
282	6	2.1	208	2	S50388	hypothetical prote	355	6	2.1	245	2	T32774	hypothetical prote
283	6	2.1	209	2	G82359	conserved hypothet	356	6	2.1	246	2	S15378	H+-transporting tw
284	6	2.1	210	2	B97984	hypothetical prote	357	6	2.1	246	2	B82764	hypothetical prote
285	6	2.1	211	2	T03685	probable superoxid	358	6	2.1	247	2	T43015	hypothetical prote
286	6	2.1	211	2	E82055	sodium-type flagel	359	6	2.1	247	2	T11654	hypothetical prote
287	6	2.1	212	2	E75334	ribonuclease H1i -	360	6	2.1	247	2	A87511	conserved hypothet
288	6	2.1	212	2	B83866	hypothetical prote	361	6	2.1	248	2	JC2581	14-3-3 protein - C
289	6	2.1	213	2	AG1450	hypothetical prote	362	6	2.1	248	2	T23759	hypothetical prote
290	6	2.1	213	1	S71287	myb-related 24.7K	363	6	2.1	248	2	S76774	thiol-disulfide in
291	6	2.1	216	2	T51730	superoxide dismuta	364	6	2.1	249	2	S78186	H+-transporting tw
292	6	2.1	216	2	I38484	olfactory receptor	365	6	2.1	249	2	H97161	cell division sept
293	6	2.1	217	2	S48021	superoxide dismuta	366	6	2.1	250	2	T01604	hypothetical prote
294	6	2.1	217	2	T36216	spda protein - Str	367	6	2.1	250	2	T49221	hypothetical prote
295	6	2.1	218	2	H84681	probable copper/zi	368	6	2.1	250	2	AF1095	conserved hypothet
296	6	2.1	218	2	A33136	proline/arginine-r	369	6	2.1	250	2	A11458	conserved hypothet
297	6	2.1	218	2	T49841	hypothetical prote	370	6	2.1	251	2	AB1105	conserved hypothet
298	6	2.1	218	2	T01104	disease resistance	371	6	2.1	251	2	AB1467	conserved hypothet
299	6	2.1	220	2	H42590	M2L protein - vacc	372	6	2.1	251	2	D83855	hypothetical prote
300	6	2.1	220	2	A87552	hypothetical prote	373	6	2.1	252	2	T01947	probable membrane
301	6	2.1	221	2	AG3570	nickel transport s	374	6	2.1	252	2	S74884	hypothetical prote
302	6	2.1	222	1	DSSPC2	superoxide dismuta	375	6	2.1	252	2	F72560	hypothetical prote
303	6	2.1	223	2	S62192	probable thymidyla	376	6	2.1	252	2	A49232	outer membrane pro
304	6	2.1	224	2	T05766	peptidylprolyl iso	377	6	2.1	253	2	T22590	hypothetical prote
305	6	2.1	224	2	C48652	transfer protein s	378	6	2.1	253	2	C86325	T29M8.5 protein -
306	6	2.1	226	2	T08335	hypothetical prote	379	6	2.1	255	2	JQ2288	SPCP2 protein - so
307	6	2.1	226	2	I39594	exeb protein - Aer	380	6	2.1	256	2	C85669	trans-2-enoyl-ACP
308	6	2.1	227	2	S68133	H+-transporting tw	381	6	2.1	256	2	AD2734	bira bifunctional
309	6	2.1	227	2	E69203	probable thymidyla	382	6	2.1	256	2	F75515	bira protein (AF20
310	6	2.1	228	2	T12799	conserved hypothet	383	6	2.1	256	2	T52051	probable aldehyde
311	6	2.1	228	2	B69777	hypothetical prote	384	6	2.1	258	2	F81022	probable ABC trans
312	6	2.1	229	2	F83534	arginine/ornithine	385	6	2.1	258	2	G75372	conserved hypothet
313	6	2.1	229	2	T44455	hypothetical prote	386	6	2.1	259	2	T01008	ribonuclease/EC 3
314	6	2.1	229	2	A05196	hypothetical prote	387	6	2.1	259	2	T22862	hypothetical prote
315	6	2.1	229	2	T06346	chloroplast envelo	388	6	2.1	260	2	H83844	hypothetical prote
316	6	2.1	229	2	F82553	hypothetical prote	389	6	2.1	260	2	H96919	ABC transporter, A
317	6	2.1	230	1	C65097	hypothetical 25.5	390	6	2.1	262	2	H70953	hypothetical prote
318	6	2.1	230	2	AC2934	aspartate racemase	391	6	2.1	263	2	C81709	conserved hypothet
319	6	2.1	230	2	H91124	hypothetical prote	392	6	2.1	265	1	G69084	conserved hypothet
320	6	2.1	230	2	G85969	hypothetical prote	393	6	2.1	265	1	T36396	probable short cha
321	6	2.1	230	2	C71337	conserved hypothet	394	6	2.1	265	2	S38581	allergen Hel 1 I p

395	6	2.1	266	2	A82851	chaperone protein	468	2.1	306	2	AE2042	ribosomal protein
396	6	2.1	266	2	T36287	probable integral	469	2.1	306	2	G64820	probable oligopept
397	6	2.1	266	2	H71521	probable metal dep	470	2.1	306	2	A85593	probable transport
398	6	2.1	266	2	B87994	protein Y71A12C.2	471	2.1	306	2	F90742	probable transport
399	6	2.1	266	2	T37362	hypothetical prote	472	2.1	306	2	AF0603	hypothetical ABC t
400	6	2.1	267	2	A30252	sugar ABC transpor	473	2.1	306	2	G83152	hypothetical prote
401	6	2.1	267	2	A32122	dolichyl-phosphate	474	2.1	307	2	T25060	hypothetical prote
402	6	2.1	267	2	B72408	conserved hypotet	475	2.1	308	2	B87059	probable pseudouri
403	6	2.1	268	2	B39429	CAMP response elem	476	2.1	308	2	A70761	hypothetical prote
404	6	2.1	268	2	B37279	enhancer-binding p	477	2.1	309	2	H95850	probable rhizopine
405	6	2.1	269	2	C31030	probable structure	478	2.1	309	2	B69556	phosphate ABC tran
406	6	2.1	269	2	A86164	protein F15K9.14 [479	2.1	309	2	B75565	hypothetical prote
407	6	2.1	269	2	D85874	probable structure	480	2.1	311	2	B95202	methionyl-tRNA for
408	6	2.1	269	2	S08346	probable structure	481	2.1	311	2	B98069	methionyl-tRNA for
409	6	2.1	269	2	AD0804	probable membrane	482	2.1	311	2	T21845	hypothetical prote
410	6	2.1	270	2	S61620	probable membrane	483	2.1	311	2	H82541	conserved hypotet
411	6	2.1	272	2	H81004	hypothetical prote	484	2.1	311	2	A97923	hypothetical prote
412	6	2.1	272	2	A81360	Protein gp17 [act	485	2.1	313	2	T20812	hypothetical prote
413	6	2.1	273	2	A37488	hypothetical 30.9K	486	2.1	313	2	T18092	hypothetical prote
414	6	2.1	273	2	A12705	conserved hypotet	487	2.1	314	2	S55210	meiotic recombina
415	6	2.1	273	2	F86665	ABC transporter pe	488	2.1	314	2	E81064	cellulite resistan
416	6	2.1	273	2	D98348	hypothetical prote	489	2.1	314	2	H70723	hypothetical prote
417	6	2.1	274	2	S07999	chlorophyll a/b-bi	490	2.1	315	2	I39479	hypothetical prote
418	6	2.1	274	2	S60270	chlorophyll a/b bi	491	2.1	316	2	H95389	probable ABC Trans
419	6	2.1	274	2	H70900	hypothetical prote	492	2.1	317	2	T15843	hypothetical prote
420	6	2.1	275	2	B49394	translation elonga	493	2.1	318	2	T02998	sigma-E factor reg
421	6	2.1	275	2	S76233	transcription term	494	2.1	318	2	AG0829	sigma-E factor reg
422	6	2.1	275	2	S44823	F54F2.9 protein -	495	2.1	320	2	JC1171	muscle regulatory
423	6	2.1	276	2	AF0402	transketolase [EC	496	2.1	320	2	S73124	hypothetical prote
424	6	2.1	276	2	T51685	myb-related transc	497	2.1	322	2	G87257	porphobilinogen de
425	6	2.1	279	2	H82997	conserved hypotet	498	2.1	322	2	AD0387	protein-export mem
426	6	2.1	280	2	T50554	3-methyl-2-oxobuta	499	2.1	325	2	A95958	probable periplasm
427	6	2.1	281	2	E07076	probable panB prot	500	2.1	325	2	D82662	hypothetical prote
428	6	2.1	281	2	T29464	hypothetical prote	501	2.1	326	2	A32273	MHC class I histoc
429	6	2.1	282	2	T06637	hypothetical prote	502	2.1	326	2	D83483	probable metal tra
430	6	2.1	282	2	AG1534	hypothetical prote	503	2.1	327	2	D90013	hypothetical prote
431	6	2.1	282	2	B20383	hypothetical prote	504	2.1	327	2	D82678	transcription regu
432	6	2.1	283	1	JQ1637	nonstructural prot	505	2.1	327	2	B36505	oxaloacetate decar
433	6	2.1	284	1	JG2526	deoxyribonuclease	506	2.1	327	2	AB0888	hypothetical prote
434	6	2.1	286	2	E87113	hypothetical prote	507	2.1	328	2	H84061	ferriochrome ABC tr
435	6	2.1	286	2	QJ1548	hypothetical 32.5K	508	2.1	328	2	AB1781	hypothetical prote
436	6	2.1	287	2	F82265	conserved hypotet	509	2.1	328	2	AC1405	hypothetical prote
437	6	2.1	288	2	T36224	dihydropterate sy	510	2.1	329	2	T14556	hypothetical prote
438	6	2.1	288	2	G81209	cell-binding facto	511	2.1	329	2	E90417	conserved hypotet
439	6	2.1	289	2	C87019	hypothetical prote	512	2.1	331	2	D70247	conserved hypotet
440	6	2.1	289	2	S92271	ribonuclease [SC 3	513	2.1	332	1	DEHULC	L-lactate dehydrog
441	6	2.1	289	2	B87514	metallo-beta-lacta	514	2.1	332	2	B87356	sugar ABC transpor
442	6	2.1	289	2	G83029	hypothetical prote	515	2.1	332	2	G72767	hypothetical prote
443	6	2.1	290	2	E70703	probable usPA prot	516	2.1	333	2	A41881	collagenase FRC (
444	6	2.1	290	2	G75470	conserved hypotet	517	2.1	333	2	T19889	hypothetical prote
445	6	2.1	290	2	JC5017	calcium-modulating	518	2.1	335	2	E90014	hypothetical prote
446	6	2.1	291	2	T30267	sugar transport pr	519	2.1	336	2	C69811	nitric-oxide synth
447	6	2.1	291	2	T00855	hypothetical prote	520	2.1	336	2	T41118	hypothetical prote
448	6	2.1	291	2	C71877	hypothetical prote	521	2.1	336	2	T20854	hypothetical prote
449	6	2.1	292	2	T36879	hypothetical prote	522	2.1	336	2	AH3010	hypothetical prote
450	6	2.1	293	2	B70455	thiosulfate sulfur	523	2.1	336	2	F98273	iron(III) dicitrat
451	6	2.1	294	2	S13141	hypothetical prote	524	2.1	337	2	AG0892	probable glycoprot
452	6	2.1	294	2	F97110	permease component	525	2.1	337	2	AG5023	CMP-stalic acid tr
453	6	2.1	296	2	H83400	cytochrome o ubiqu	526	2.1	337	2	AG0963	hypothetical prote
454	6	2.1	296	2	S47594	cyclophilin B-bind	527	2.1	337	2	T04035	hypothetical prote
455	6	2.1	297	2	H51332	hypothetical prote	528	2.1	338	1	TVMSFB	transforming prote
456	6	2.1	297	2	D87260	integral membrane	529	2.1	338	2	S52284	lumicon, secretory
457	6	2.1	299	2	E70842	probable acid phos	530	2.1	338	2	S06659	hypothetical prote
458	6	2.1	299	2	S54087	probable membrane	531	2.1	339	2	F96638	hypothetical prote
459	6	2.1	300	1	B71090	hypothetical prote	532	2.1	340	2	T37030	alcohol dehydrogen
460	6	2.1	300	2	T43205	centrosomin homolo	533	2.1	340	2	D71816	branched-chain-am
461	6	2.1	300	2	T38297	hypothetical prote	534	2.1	340	2	D64703	hypothetical prote
462	6	2.1	301	2	T29384	hypothetical prote	535	2.1	340	2	T19538	hypothetical prote
463	6	2.1	303	2	JC2410	ADP-ribosyl cyclas	536	2.1	340	2	D84109	hypothetical prote
464	6	2.1	303	2	T29383	hypothetical prote	537	2.1	341	2	S31571	cinnamyl-alcohol d
465	6	2.1	304	2	B69304	3-hydroxyacyl-CoA	538	2.1	341	2	I55623	thromboxane A2 rec
466	6	2.1	305	2	G82041	general secretion	539	2.1	341	2	F69789	hypothetical prote
467	6	2.1	305	2	G70382	phosphotidylglycer	540	2.1	341	2	AC1507	hypothetical prote

541	6	2.1	342	2	A46743	lumican precursor	614	6	2.1	369	2	AG0776	conserved hypothet
542	6	2.1	342	2	T21875	hypothetical prote	615	6	2.1	369	2	T24793	hypothetical prote
543	6	2.1	342	2	C84234	phosphate regulato	616	6	2.1	369	2	T01196	transcription fact
544	6	2.1	343	2	A49117	thromboxane A2 rec	617	6	2.1	370	2	AE0289	conserved hypothet
545	6	2.1	343	2	T16909	KHC class I RT1 C-	618	6	2.1	372	2	S67770	probable membrane
546	6	2.1	343	2	T33945	hypothetical prote	619	6	2.1	373	2	S15161	long-chain-fatty-a
547	6	2.1	343	2	G75178	membrane protein p	620	6	2.1	374	2	S55894	hypothetical prote
548	6	2.1	344	1	A40005	hyocyanine (6S)-d	621	6	2.1	376	2	AE12176	homocitrate synth
549	6	2.1	344	2	T12315	NADH2 dehydrogen	622	6	2.1	376	2	AG1410	cell division prot
550	6	2.1	344	2	T12320	NADH2 dehydrogen	623	6	2.1	376	2	T35868	probable dipeptida
551	6	2.1	344	2	T17068	NADH2 dehydrogen	624	6	2.1	376	2	S67085	hypothetical prote
552	6	2.1	344	2	C70208	conserved hypothet	625	6	2.1	377	1	PSMQCJ	gastricin (EC 3.4
553	6	2.1	345	2	T12351	NADH2 dehydrogen	626	6	2.1	377	2	T47471	cysteine proteinas
554	6	2.1	345	2	T12362	NADH2 dehydrogen	627	6	2.1	377	2	AE0845	probable rubredoxi
555	6	2.1	345	2	T17071	NADH2 dehydrogen	628	6	2.1	377	2	F97267	uncharacterized co
556	6	2.1	345	2	H72488	probable anthranil	629	6	2.1	379	2	T20394	hypothetical prote
557	6	2.1	345	2	AB1837	hypothetical prote	630	6	2.1	380	2	E70181	hypothetical prote
558	6	2.1	345	2	C72760	probable heme expo	631	6	2.1	380	2	T39015	probable DNA-J-lik
559	6	2.1	346	2	A45885	KHC class I histoc	632	6	2.1	381	2	JH0152	acid phosphatase (
560	6	2.1	346	2	T19008	hypothetical prote	633	6	2.1	381	2	B48156	translation regula
561	6	2.1	346	2	AC0187	probable iron-side	634	6	2.1	382	2	C43706	nifv protein - Azo
562	6	2.1	347	2	T35518	probable secreted	635	6	2.1	382	2	AB3215	conserved hypothet
563	6	2.1	350	2	S71923	cysteine proteinas	636	6	2.1	382	2	AB0441	alkanesulfonate mo
564	6	2.1	350	2	T37511	probable phosphor	637	6	2.1	384	2	S75683	inner membrane pro
565	6	2.1	350	2	S51494	arabinogalactan en	638	6	2.1	385	2	S29758	nifv protein - Azo
566	6	2.1	350	2	S76651	hypothetical prote	639	6	2.1	385	2	AB1656	transmembrane tran
567	6	2.1	352	2	B85709	probable DNA methy	640	6	2.1	386	2	E75588	glutaryl-CoA dehyd
568	6	2.1	352	2	D90851	probable complex	641	6	2.1	386	2	AB7697	DegT/DnrJ/BryCl/St
569	6	2.1	353	2	S71338	t-complex protein	642	6	2.1	387	2	S07259	coat protein - tom
570	6	2.1	353	2	F83570	hypothetical prote	643	6	2.1	387	2	T23915	hypothetical prote
571	6	2.1	353	2	B36963	bcsA 5' -region pro	644	6	2.1	387	2	B84365	hypothetical prote
572	6	2.1	354	2	AH3092	transcription regu	645	6	2.1	388	2	A29937	gastricin (EC 3.4
573	6	2.1	354	2	B98134	thiur protein (AF17	646	6	2.1	388	2	JC7246	pepsinogen C - com
574	6	2.1	354	2	T45837	hypothetical prote	647	6	2.1	388	2	S28798	hypothetical prote
575	6	2.1	354	2	H96928	ABC transporter, p	648	6	2.1	388	2	F70430	hypothetical prote
576	6	2.1	355	2	S17704	anthranilate phosp	649	6	2.1	389	2	A49905	protein secretion
577	6	2.1	355	2	F95979	probable transcrip	650	6	2.1	390	1	A39249	neutrophil cytosol
578	6	2.1	356	1	T01933	probable aldose 1-	651	6	2.1	390	2	AC3359	2-C-methyl-D-eryth
579	6	2.1	356	2	T21681	hypothetical prote	652	6	2.1	390	2	AC3761	penicillin binding
580	6	2.1	356	2	AH0068	UDP-N-acetylgluc	653	6	2.1	391	2	AB1285	transmembrane tran
581	6	2.1	357	2	T09141	cinnamyl-alcohol d	654	6	2.1	392	1	S18593	chloramphenicol re
582	6	2.1	357	2	T20029	hypothetical prote	655	6	2.1	392	2	D53240	allergen Amb a 1.4
583	6	2.1	358	2	T36415	probable iron-side	656	6	2.1	392	2	G96004	probable reverse t
584	6	2.1	358	2	D99823	hypothetical prote	657	6	2.1	393	2	B86189	protein T25N20.9 (
585	6	2.1	358	2	C82281	ferric vibriobacti	658	6	2.1	395	2	D70688	probable nitrate/n
586	6	2.1	359	2	D83103	probable phospholi	659	6	2.1	395	2	F82695	hypothetical prote
587	6	2.1	360	2	S59598	cysteine proteinas	660	6	2.1	396	2	E96911	glutamyl-tRNA redu
588	6	2.1	360	2	T34510	hypothetical prote	661	6	2.1	396	2	AG2881	glyd family secret
589	6	2.1	360	2	JC6057	RNA-binding protei	662	6	2.1	396	2	G97657	hypothetical prote
590	6	2.1	361	2	A41535	glutamyl-peptide	663	6	2.1	397	2	F83385	probable MFS trans
591	6	2.1	362	2	T29053	branched-chain-ami	664	6	2.1	397	2	F90411	conserved hypothet
592	6	2.1	362	2	B87571	hypothetical prote	665	6	2.1	397	2	T46710	multidrug resist
593	6	2.1	364	2	F70137	cell division prot	666	6	2.1	397	2	AE1613	multidrug-efflux t
594	6	2.1	364	2	T06507	reversibly glycosy	667	6	2.1	397	2	AI1250	multidrug-efflux t
595	6	2.1	364	2	AE0259	probable phage pro	668	6	2.1	399	2	F83633	hypothetical prote
596	6	2.1	365	2	A69593	naringenin-chalcon	669	6	2.1	400	2	AB7427	thiolase family pr
597	6	2.1	365	2	F64577	type I restriction	670	6	2.1	400	2	T33073	hypothetical prote
598	6	2.1	365	2	B4515	hypothetical prote	671	6	2.1	400	2	T18997	nicotinic acetylch
599	6	2.1	365	2	T06615	hypothetical prote	672	6	2.1	402	2	AI1853	sodium-dependent n
600	6	2.1	365	2	B24458	hypothetical prote	673	6	2.1	402	2	T35091	hypothetical prote
601	6	2.1	365	2	T50566	probable ABC-type	674	6	2.1	404	2	T03606	probable LFV flora
602	6	2.1	365	2	B84611	probable ubiquitin	675	6	2.1	405	2	T08521	tnlQ protein homol
603	6	2.1	365	2	A48105	probable M-factor	676	6	2.1	405	2	AF2559	hypothetical prote
604	6	2.1	365	2	F97674	hypothetical prote	677	6	2.1	405	2	AG2534	hypothetical prote
605	6	2.1	367	2	S23349	hypothetical prote	678	6	2.1	406	2	T36632	probable oxidoredu
606	6	2.1	367	2	A54357	muconate cyclisom	679	6	2.1	407	2	T02670	probable thromboxa
607	6	2.1	368	2	C70786	probable ilvE prot	680	6	2.1	407	2	T00214	type II secretion
608	6	2.1	368	2	T44887	probable branched-	681	6	2.1	407	2	AE0121	probable membrane
609	6	2.1	368	2	AE2846	Ca2+/H+ antiporter	682	6	2.1	409	2	JC7293	activated T cell t
610	6	2.1	368	2	AD2899	conserved hypothet	683	6	2.1	410	2	JC4287	cytochrome P450 sc
611	6	2.1	368	2	B97623	cpaA protein (AJ00	684	6	2.1	410	2	F88978	protein F37B4.4 li
612	6	2.1	369	2	F69478	NADH2 dehydrogen	685	6	2.1	410	2	H71125	hypothetical prote
613	6	2.1	369	2	A53959	thromboxane A-2 re	686	6	2.1	411	2	F87644	transcription regu

687	6	2.1	411	2	F84135	multidrug-efflux t	760	6	2.1	453	2	B83427	pata-aminobenzoate
688	6	2.1	412	2	A82444	GDH family prote	761	6	2.1	453	2	E83953	D-serine/b-alanine
689	6	2.1	413	2	A2360	hypothetical prote	762	6	2.1	453	2	A33597	C4-dicarboxylate t
690	6	2.1	414	2	A97542	D-ala-D-ala-carbox	763	6	2.1	453	2	S53995	tox protein - Pse
691	6	2.1	414	2	E70514	probable cys2 - M	764	6	2.1	453	2	A95946	probable reverse t
692	6	2.1	414	2	A12544	hypothetical prote	765	6	2.1	454	2	A75444	hypothetical prote
693	6	2.1	414	2	H87191	low-affinity inorg	766	6	2.1	454	2	S77005	sensory transducti
694	6	2.1	414	2	A69907	cell wall-binding	767	6	2.1	454	2	C75472	probable lipase -
695	6	2.1	414	2	B96905	hypothetical prote	768	6	2.1	455	2	A12409	cytochrome P450 li
696	6	2.1	415	1	A8359	glutamyl-cRNA redu	769	6	2.1	455	2	T34412	hypothetical prote
697	6	2.1	415	2	H95412	hypothetical prote	770	6	2.1	456	1	I40516	spar protein Bac
698	6	2.1	416	2	T22514	hypothetical prote	771	6	2.1	456	2	A84196	acyl-CoA dehydroge
699	6	2.1	417	1	A49684	gastric intrinsic	772	6	2.1	456	2	F83317	adenylosuccinate l
700	6	2.1	418	2	T36358	hypothetical prote	773	6	2.1	456	2	T51117	hypothetical prote
701	6	2.1	419	2	S54102	isopenicillin N ep	774	6	2.1	457	2	I73636	neuroal olfactome
702	6	2.1	419	2	B54613	hypothetical prote	775	6	2.1	458	2	A57397	chondroitin 6-sulf
703	6	2.1	419	2	F19000	hypothetical prote	776	6	2.1	458	2	T49114	hypothetical prote
704	6	2.1	421	2	F87040	conserved hypotet	777	6	2.1	459	2	T11084	NADH2 dehydrogenas
705	6	2.1	421	2	T25383	hypothetical prote	778	6	2.1	459	2	A89785	hexose phosphate t
706	6	2.1	421	2	F95371	conserved hypotet	779	6	2.1	460	2	A10689	probable amino aci
707	6	2.1	422	2	A71542	probable glutamate	780	6	2.1	460	2	A82049	conserved hypotet
708	6	2.1	423	2	C72561	hypothetical prote	781	6	2.1	463	2	JC2307	ribulose-bisphosph
709	6	2.1	424	2	T05775	GI/S transition co	782	6	2.1	463	2	D95019	hypothetical prote
710	6	2.1	425	2	I56329	gene D3 protein -	783	6	2.1	463	2	F83396	conserved hypotet
711	6	2.1	425	2	A37912	thrombin receptor	784	6	2.1	464	2	C70414	NADH2 dehydrogenas
712	6	2.1	426	2	F95846	probable ABC trans	785	6	2.1	464	2	E83834	flagellin BH1477 l
713	6	2.1	426	2	B90410	hypothetical prote	786	6	2.1	464	2	F97714	hypothetical prote
714	6	2.1	427	2	H72678	hypothetical prote	787	6	2.1	465	2	F71213	probable H(+)-tran
715	6	2.1	427	2	S17148	alpha-thrombin rec	788	6	2.1	465	2	C75028	h+-transporting AT
716	6	2.1	430	2	B3572	peptidyl-prolyl ci	789	6	2.1	467	2	A12231	nicotinamide nucle
717	6	2.1	430	2	A82316	hypothetical prote	790	6	2.1	467	2	AB3418	sensory transducti
718	6	2.1	431	2	F97318	acyl-CoA thioester	791	6	2.1	468	2	T07055	probable potassium
719	6	2.1	431	2	A2470	hypothetical prote	792	6	2.1	468	2	F84644	hypothetical prote
720	6	2.1	431	2	S09824	hypothetical prote	793	6	2.1	469	2	JC5741	membrane-bound pro
721	6	2.1	432	2	T17829	ankyrin repeat pro	794	6	2.1	470	2	F36953	dihydropolamide d
722	6	2.1	432	2	T08771	hypothetical prote	795	6	2.1	471	2	S29039	Na+-transporting A
723	6	2.1	433	2	A28055	K-kininogen, LMW I	796	6	2.1	471	2	AG0145	probable Pyridoxal
724	6	2.1	433	2	A00909	oxaloacetate decar	797	6	2.1	471	2	D83388	probable MFS trans
725	6	2.1	433	2	A10508	hypothetical prote	798	6	2.1	472	2	A12997	transcription regu
726	6	2.1	433	2	T39745	pyrimidine-nucleos	799	6	2.1	472	2	AG3600	cellulose synthase
727	6	2.1	434	2	B72228	serotonin receptor	800	6	2.1	473	2	F82561	hemolysin secretio
728	6	2.1	436	2	UN0591	UDP-N-acetylglucos	801	6	2.1	473	2	B82765	conserved hypotet
729	6	2.1	436	2	A96642	5-hydroxytryptamin	802	6	2.1	474	2	H90582	preprotein translo
730	6	2.1	437	2	I57942	gamma-glutamyl pho	803	6	2.1	474	2	T36685	probable sodium/pr
731	6	2.1	438	2	A20076	two-component hybr	804	6	2.1	475	2	A81735	cysteineyl-tRNA syn
732	6	2.1	438	2	A1886	hypothetical prote	805	6	2.1	475	2	E84745	probable splicing
733	6	2.1	439	2	T18898	hypothetical prote	806	6	2.1	476	2	JC7304	gene P3 protein -
734	6	2.1	439	2	A12098	hypothetical prote	807	6	2.1	477	2	S01696	fatty acid hydrope
735	6	2.1	440	2	JC5520	serotonin receptor	808	6	2.1	477	2	AB3647	melittin resistanc
736	6	2.1	441	2	C96032	C4-dicarboxylate t	809	6	2.1	478	2	D66990	transmembrane prot
737	6	2.1	441	2	T4591	hypothetical prote	810	6	2.1	479	1	A43241	glycine hydroxymet
738	6	2.1	443	2	A00028	preprotein translo	811	6	2.1	479	2	B87699	conserved hypotet
739	6	2.1	443	2	D64161	hypothetical prote	812	6	2.1	480	2	S74228	fatty acid hydrope
740	6	2.1	443	2	T30556	stamina pistilloid	813	6	2.1	482	2	H98285	probable transcrip
741	6	2.1	444	2	S27384	C4-dicarboxylate t	814	6	2.1	483	2	T35715	export protein - S
742	6	2.1	444	2	T72734	hypothetical prote	815	6	2.1	483	2	S52974	regulatory protein
743	6	2.1	444	2	T19855	hypothetical prote	816	6	2.1	484	2	T34016	hypothetical prote
744	6	2.1	445	1	S74826	NADH2 dehydrogenas	817	6	2.1	484	2	E82248	fatty oxidation co
745	6	2.1	445	2	S6207	EMP47 protein prec	818	6	2.1	484	2	T25944	hypothetical prote
746	6	2.1	447	2	F84373	hypothetical prote	819	6	2.1	485	2	I73637	neuroal olfactome
747	6	2.1	448	2	AD2962	C4-dicarboxylate t	820	6	2.1	485	2	C75460	hypothetical prote
748	6	2.1	448	2	B98321	C4-dicarboxylate t	821	6	2.1	486	2	A89927	elastin binding pr
749	6	2.1	448	2	T32643	hypothetical prote	822	6	2.1	487	2	S54265	stage V sporulatio
750	6	2.1	448	2	G95416	probable response	823	6	2.1	487	2	G83827	glycoprotein GC -
751	6	2.1	448	2	D86368	hypothetical prote	824	6	2.1	488	2	C72334	hypothetical prote
752	6	2.1	448	2	A81379	probable oxidoredu	825	6	2.1	488	2	A69344	hypothetical prote
753	6	2.1	449	2	F86852	amino acid permeas	826	6	2.1	488	2	F97039	glutamate synthase
754	6	2.1	449	2	S71005	glutamate transpor	827	6	2.1	489	2	AC1663	probable cytochrom
755	6	2.1	449	2	A53634	nitric-oxide reduc	828	6	2.1	490	2	T06710	probable cytochrom
756	6	2.1	450	2	F95360	probable transmemb	829	6	2.1	490	2	T06711	probable cytochrom
757	6	2.1	450	2	T21931	hypothetical prote	830	6	2.1	490	2	A87672	tldD protein limpo
758	6	2.1	451	2	H5559	conserved hypotet	831	6	2.1	490	2	H71480	probable GTPase/GT
759	6	2.1	451	2	H9798	conserved hypotet	832	6	2.1	490	2	A61744	GTP-binding protei

833	6	2.1	491	2	AC2233	hypothetical prote	906	6	2.1	539	2	AH1035	probable phage tai
834	6	2.1	493	2	G83842	stage V sporulatio	907	6	2.1	541	1	A70022	multidrug-efflux t
835	6	2.1	494	2	S16068	testosterone 15alp	908	6	2.1	542	2	D30944	hypothetical prote
836	6	2.1	494	2	B33531	cytochrome P450 2A	909	6	2.1	542	2	H85792	hypothetical prote
837	6	2.1	494	2	A33531	testosterone 15alp	910	6	2.1	542	2	G64942	hypothetical prote
838	6	2.1	495	2	S32179	tniQ protein homol	911	6	2.1	544	2	A70155	inner membrane pro
839	6	2.1	496	2	S43114	alderyde dehydrog	912	6	2.1	545	2	C90047	hypothetical prote
840	6	2.1	496	2	F84664	hypothetical prote	913	6	2.1	545	2	E30460	hypothetical prote
841	6	2.1	496	2	T30976	hypothetical prote	914	6	2.1	545	2	C95409	conserved hypotnet
842	6	2.1	497	2	S75708	hypothetical prote	915	6	2.1	546	2	H72357	hypothetical prote
843	6	2.1	497	2	S22708	homectic protein e	916	6	2.1	547	2	T23614	hypothetical prote
844	6	2.1	498	2	AH0952	conserved hypotnet	917	6	2.1	549	2	T15506	hypothetical prote
845	6	2.1	499	2	S46860	wetA protein - Pen	918	6	2.1	551	2	A49904	L-lactate permease
846	6	2.1	501	2	T44298	sodium/proline sym	919	6	2.1	551	2	A98189	L-lactate permease
847	6	2.1	502	1	D64110	lysine-tRNA ligase	920	6	2.1	551	2	B36036	L-lactate permease
848	6	2.1	502	1	ACHUA7	nicotinic acetylch	921	6	2.1	551	2	S36283	protein-tyrosine-p
849	6	2.1	502	2	JN0113	nicotinic acetylch	922	6	2.1	552	2	A39493	hypothetical prote
850	6	2.1	502	2	G02359	alpha 7 neuronal n	923	6	2.1	553	2	E95160	hypothetical prote
851	6	2.1	502	2	T25669	hypothetical prote	924	6	2.1	553	2	D98026	hypothetical prote
852	6	2.1	503	2	E82730	peptide synthase X	925	6	2.1	554	2	D72760	hypothetical prote
853	6	2.1	504	2	T37984	probable homoserin	926	6	2.1	554	2	H71128	hypothetical prote
854	6	2.1	504	2	E64118	sodium/proline sym	927	6	2.1	555	2	S63177	hypothetical prote
855	6	2.1	505	2	T10896	cytochrome P450 (E	928	6	2.1	557	2	B28182	hemolysin B - Serr
856	6	2.1	505	2	D96672	probable Cytochrom	929	6	2.1	558	2	S71337	t-complex protein
857	6	2.1	506	2	H83831	sopre germination	930	6	2.1	559	2	T23571	hypothetical prote
858	6	2.1	506	2	B87102	conserved membrane	931	6	2.1	560	2	T14616	hypothetical prote
859	6	2.1	506	2	T40396	glucosyltransferas	932	6	2.1	561	2	A52649	alpha-glucosidase
860	6	2.1	506	2	H91214	probable 2-compone	933	6	2.1	561	2	AH0452	hemolysin activato
861	6	2.1	506	2	T47184	hypothetical prote	934	6	2.1	561	2	C84721	hypothetical prote
862	6	2.1	506	2	A86061	probable 2-compone	935	6	2.1	563	2	S32156	mandelonitrile lya
863	6	2.1	506	2	C65178	hypothetical 57.4	936	6	2.1	564	2	H86278	Fl14L17.20 protein
864	6	2.1	507	2	S33921	alpha-amyase (EC	937	6	2.1	564	2	E82539	ABC transporter At
865	6	2.1	510	2	A96673	probable cytochrom	938	6	2.1	566	2	F70028	transmembrane rece
866	6	2.1	510	2	AG1539	oligo-1,6-glucosid	939	6	2.1	566	2	S28068	mxid protein - Shi
867	6	2.1	510	2	B88381	protein T22P7.1 fi	940	6	2.1	569	2	AC0998	probable membrane
868	6	2.1	511	2	H96672	probable cytochrom	941	6	2.1	570	2	F87446	potassium-transport
869	6	2.1	511	2	T10964	inositol-3-phospha	942	6	2.1	571	2	G80891	probable sulfatase
870	6	2.1	511	2	T04221	hypothetical prote	943	6	2.1	571	2	B85726	probable sulfatase
871	6	2.1	512	2	E84501	probable cytochrom	944	6	2.1	571	2	E64903	arylsulfatase homo
872	6	2.1	512	2	T06716	hypothetical prote	945	6	2.1	573	2	T07948	mandelonitrile lya
873	6	2.1	516	2	JE0266	L-amino-acid oxida	946	6	2.1	573	2	AG2133	ATP-binding protei
874	6	2.1	517	2	S69347	steroid ilbeta-mon	947	6	2.1	574	2	H86467	probable transcrip
875	6	2.1	518	2	H64775	probable membrane	948	6	2.1	575	2	G75282	probable glucathio
876	6	2.1	518	2	B85543	hypothetical prote	949	6	2.1	576	2	B71420	hypothetical prote
877	6	2.1	518	2	F90692	hypothetical prote	950	6	2.1	577	2	S64613	probable membrane
878	6	2.1	520	2	AI3596	sugar transport AT	951	6	2.1	578	2	T01229	hypothetical prote
879	6	2.1	521	1	VHBPT4	major capsid prote	952	6	2.1	579	2	A56740	sperm-egg recognit
880	6	2.1	521	2	T35832	probable integral	953	6	2.1	580	2	B38418	jockey protein 1 -
881	6	2.1	521	2	E95052	hypothetical prote	954	6	2.1	581	2	S44896	ZK1236.1 protein -
882	6	2.1	523	2	S53401	probable membrane	955	6	2.1	581	2	A97119	probable membrane
883	6	2.1	524	1	DEYCG6	glucose-6-phospat	956	6	2.1	581	2	S46742	hypothetical prote
884	6	2.1	524	2	T43649	hypothetical prote	957	6	2.1	582	2	S24545	intermediate filam
885	6	2.1	525	2	T43649	chaperonin CCT4 -	958	6	2.1	583	2	JC6504	alpha,alpha-trehal
886	6	2.1	526	2	S03600	cell surface antig	959	6	2.1	583	2	B82744	conserved hypotnet
887	6	2.1	527	2	S64702	cell surface antig	960	6	2.1	586	2	S57195	conserved hypotnet
888	6	2.1	527	2	T39263	chaperonin subunit	961	6	2.1	586	2	T12886	conserved hypotnet
889	6	2.1	527	2	T37055	probable oxidoredu	962	6	2.1	590	2	A82350	probable phosphol
890	6	2.1	527	2	T25131	hypothetical prote	963	6	2.1	590	2	F95853	hypothetical prote
891	6	2.1	528	2	C85056	probable DNA-bindi	964	6	2.1	591	2	D85063	hypothetical prote
892	6	2.1	529	1	SAHUP	cell surface antig	965	6	2.1	591	2	T13650	zinc finger protei
893	6	2.1	529	2	H70724	hypothetical prote	966	6	2.1	592	2	T42078	serine/threonine p
894	6	2.1	532	2	T07927	protein disulfide-	967	6	2.1	593	2	S38145	uroporphyrinogen m
895	6	2.1	532	2	T28784	hypothetical prote	968	6	2.1	593	2	I39173	A kinase anchor pr
896	6	2.1	533	2	E94858	phosphoprotein pho	969	6	2.1	594	2	D97431	probable alpha-glu
897	6	2.1	533	2	JC2285	preproteint translo	970	6	2.1	594	2	T38114	pyruvate decarboxy
898	6	2.1	533	2	H70735	hypothetical prote	971	6	2.1	594	2	T23841	hypothetical prote
899	6	2.1	533	2	G72593	hypothetical prote	972	6	2.1	595	2	A48658	flagellin - Escher
900	6	2.1	535	2	G97255	CTP synthase (UTP	973	6	2.1	595	2	B48658	flagellin - Escher
901	6	2.1	536	2	H62880	probable ABC subst	974	6	2.1	595	2	S75439	hypothetical prote
902	6	2.1	537	1	YRMSB6	tyrosinase-related	975	6	2.1	595	2	T04438	hypothetical prote
903	6	2.1	537	2	C97765	CTP synthase (EC 6	976	6	2.1	597	2	E70928	hypothetical prote
904	6	2.1	538	2	AC1850	NADH dehydrogenase	977	6	2.1	600	2	T50799	serine/threonine p
905	6	2.1	538	2	S67766	RNA-export mediato	978	6	2.1	600	2	T02692	hypothetical prote

979 6 2.1 601 2 AH1003 glutathione-regula
 980 6 2.1 602 2 T45386 endopeptidase IV [
 981 6 2.1 604 2 C87818 protein gln-1 limp
 982 6 2.1 604 2 T15132 ATP-dependent RNA
 983 6 2.1 605 2 D83007 regulatory protein
 984 6 2.1 606 2 AH2485 hypothetrical prote
 985 6 2.1 608 2 S76192 hypothetrical prote
 986 6 2.1 609 2 T04946 hypothetrical prote
 987 6 2.1 610 2 T23836 hypothetrical prote
 988 6 2.1 613 1 S74461 ABC transporter sl
 989 6 2.1 614 2 H83978 GTP-binding protei
 990 6 2.1 618 2 S33044 hypothetrical prote
 991 6 2.1 620 1 WZBEC1 gene 28 protein -
 992 6 2.1 620 2 S19660 dnaK-type molecula
 993 6 2.1 620 2 S73236 dnaK-type molecula
 994 6 2.1 621 2 A84933 glutamine-fructose
 995 6 2.1 621 2 A83016 Na+/H+ antiporter
 996 6 2.1 622 2 G81981 probable lipopolys
 997 6 2.1 623 2 I46382 ZPI precursor - mo
 998 6 2.1 623 2 B81037 lipopolysaccharide
 999 6 2.1 624 2 A35576 collagen alpha 2(X
 1000 6 2.1 625 2 S68434 FMEamide-activate

ALIGNMENTS

RESULT 1

B38290
 GRO-gamma precursor - human
 N:Alternate names: growth-regulated protein gamma; macrophage inflammatory protein 2 beta
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1991 #sequence_revision 27-Oct-1995 #text_change 20-Aug-1999
 C:Accession: JH0282; B38290; C46519
 R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van De
 J. Exp. Med. 172, 911-919, 1990
 A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
 A:Reference number: JH0200; MUID:90354792; PMID:2201751
 A:Accession: JH0282
 A:Molecule type: mRNA
 A:Residues: 1-107 <TEK>
 A:Cross-references: GB:X53800; NID:G34662; PIDN:CAA37809.1; PID:G34663
 R:Hasikill, S.; Pearce, A.; Morris, J.; Sporn, S.A.; Anisowicz, G.; Billiau, A.; Van Damme,
 Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
 A:Title: Identification of three related human GRO genes encoding cytokine functions.
 A:Reference number: A38290; MUID:91017578; PMID:2217207
 A:Accession: B38290
 A:Molecule type: mRNA
 A:Residues: 1-26,'G',29-107 <HAS>
 A:Cross-references: GB:M36821; NID:G183632; PIDN:AAA63184.1; PID:G183633
 R:Proost, P.; De Wolf-Peters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
 J. Immunol. 150, 1000-1010, 1993
 A:Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tu
 A:Reference number: A46519; MUID:93139489; PMID:8423327
 A:Accession: C46519
 A:Molecule type: protein
 A:Residues: 35-52 <PRO>
 A:Experimental source: MG-63 osteosarcoma cells
 C:Genetics:
 A:Map position: 4q21
 C:Superfamily: beta-thromboglobulin
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-107/Product: GRO-gamma #status experimental <MAT>

Query Match 2.8%; Score 8; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAAAS 174

| | | | |

22 LLLLVAAAS 29

DB

RESULT 2

JH0281
 macrophage inflammatory protein 2 alpha precursor - human
 N:Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
 C:Accession: JH0281; A35931; A38290; A60407
 R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van De
 J. Exp. Med. 172, 911-919, 1990
 A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
 A:Reference number: JH0200; MUID:90354792; PMID:2201751
 A:Accession: JH0281
 A:Molecule type: mRNA
 A:Residues: 1-107 <TEK>
 A:Cross-references: GB:X53799; NID:G34658; PIDN:CAA37808.1; PID:G34659
 R:Ida, N.; Grotendorst, G.R.
 Mol. Cell. Biol. 10, 5596-5599, 1990
 A:Title: Cloning and sequencing of a new gro transcript from activated human monocytes:
 A:Reference number: A35931; MUID:90377259; PMID:2078213
 A:Accession: A35931
 A:Molecule type: mRNA
 A:Residues: 1-107 <IID>
 A:Cross-references: GB:M57731; GB:M36964; NID:G183626; PIDN:AAA63182.1; PID:G183627
 R:Hasikill, S.; Pearce, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; N
 Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
 A:Title: Identification of three related human GRO genes encoding cytokine functions.
 A:Reference number: A38290; MUID:91017578; PMID:2217207
 A:Accession: A38290
 A:Molecule type: mRNA
 A:Residues: 1-107 <HAS>
 A:Cross-references: GB:M36820; NID:G183628; PIDN:AAA63183.1; PID:G183629
 R:Sporn, S.A.; Bierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Hasikill,
 J. Immunol. 144, 4434-4441, 1990
 A:Title: Monocyte adherence results in selective induction of novel genes sharing homolo
 A:Reference number: A60407; MUID:90257367; PMID:2341726
 A:Accession: A60407
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 56-107 <SPO>
 C:Superfamily: beta-thromboglobulin
 C:Keywords: inflammation
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 2.8%; Score 8; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAAAS 174

| | | | |

22 LLLLVAAAS 29

DB

RESULT 3

AI2439
 hypothetrical protein all5073 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AI2439
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AI2439
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-475 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076772.1; PID:G1713421.1; PID:G1713421.1; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all5073

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Query Match      2.8%; Score 8; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LTLVLLLF 11
Db      130 LTLVLLLF 137

RESULT 4
C90171
RNase L inhibitor [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: C90171
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90171
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-600 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813430; PIDN:AAK40626.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS00287
C:Superfamily: ribonuclease L inhibitor; ATP-binding cassette homology; ferredoxin 2[4Fe

Query Match      2.8%; Score 8; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 10;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 LLVAASLL 176
Db      221 LLVAASLL 228

RESULT 5
C30552
macrophage inflammatory protein 1-beta precursor - mouse
N:Alternate names: H400; SIS gamma; T-cell activation protein gamma
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 16-Jul-1999
C:Accession: C30552; J00088; F80304; S22042
R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a ne
s of various activation processes.
A:Reference number: A30552; MUID:89093958; PMID:2521353
A:Accession: C30552
A:Molecule type: mRNA
A:Residues: 1-92 <BRO>
A:Cross-references: GB:M23503; NID:G533244; PIDN:AAA40148.1; PID:G533245
R:Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Ma
J. Exp. Med. 168, 2251-2259, 1988
A:Title: Resolution of the two components of macrophage inflammatory protein 1, and clon
A:Reference number: J00088; MUID:89067830; PMID:3059856
A:Accession: J00088
A:Molecule type: mRNA
A:Residues: 1-92 <SHE>
A:Cross-references: GB:M35590; NID:g199696; PIDN:AAA39708.1; PID:g199697
A:Accession: F80304
A:Molecule type: protein
A:Residues: 24-33, 'XX', '36', 'X', '38 <SH2>
R:Daubersies, P.; Lepretre, F.; Baillet, B.; Grove, M.; Pragnell, I.; Plumb, M.
submitted to the EMBL Data Library, October 1991
A:Description: Sequence of the murine macrophage inflammatory protein 1b gene.
A:Reference number: S22042
A:Accession: S22042
A>Status: preliminary

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A:Molecule type: DNA
A:Residues: 1-92 <DAU>
A:Cross-references: EMBL:X62502; NID:G53126; PIDN:CAA44364.1; PID:G53127
C:Comment: This protein is a monokine.
C:Genetics:
A:Introns: 26/1; 64/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      2.4%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 22;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 LLLLVA 173
Db      10 LLLLVA 16

RESULT 6
D90259
hypothetical protein SSO1068 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: D90259
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90259
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <KUR>
A:Cross-references: GB:AE006641; NID:gi3814257; PIDN:AAK41331.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1068

```

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Query Match      2.4%; Score 7; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 23;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLTLVL 8
Db      68 PLTLVL 74

RESULT 7
A28414
melanoma growth-stimulatory activity precursor - human
N:Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha; gr
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C:Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
R:Baker, N.E.; Kucera, G.; Richmond, A.
Nucleic Acids Res. 18, 6453, 1990
A:Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) ge
A:Reference number: S13669; MUID:91057157; PMID:2128556
A:Accession: S13669
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <BAK>
A:Cross-references: EMBL:X54489; NID:g34625; PIDN:CAA38361.1; PID:g34626
R:Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A:Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A:Reference number: A94184; MUID:88041072; PMID:2890161
A:Accession: A28414
A:Molecule type: mRNA
A:Residues: 1-107 <ANI>

```

A;Cross-references: GB:J03561; NID:q183622; PIDN:AAA35933.1; PID:q306806
R;Richmond, A.; Balentien, E.; Thomas, H.G.; Flaggs, G.; Barton, D.E.; Spiess, J.; Bordo
EMBO J. 7, 2025-2033, 1988
A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimulat
A;Reference number: S00983; MUID:88328991; PMID:2970963
A;Accession: S00983
A;Molecule type: mRNA
A;Residues: 1-107 <RIC>
A;Cross-references: EMBL:X12510; NID:g34621; PIDN:CAA31027.1; PID:g34622
R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preisner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-
A;Reference number: A60401; MUID:90187866; PMID:2179408
A;Accession: B60401
A;Molecule type: protein
A;Residues: 35-42, 'X', 44, 'X', 46-48 <SCH>
A;Experimental source: dermal fibroblasts
R;Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neut
A;Reference number: S03975; MUID:89246368; PMID:2655583
A;Accession: S03976
A;Molecule type: protein
A;Residues: 35-41, 'X', 43-49, 'X', 51-52, 'XX', 55-57 <GOL>
R;Schroeder, J.M.; Persoon, N.L.M.; Christophers, E.
J. Exp. Med. 171, 1091-1100, 1990
A;Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil-ad
nity with melanoma growth stimulatory activity.
A;Reference number: A47626; MUID:90217938; PMID:2182761
A;Accession: A47626
A;Molecule type: protein
A;Residues: 35-63, 'X', 65 <SC2>
A;Experimental source: LPS-stimulated monocytes
R;Probst, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
J. Immunol. 150, 1000-1010, 1993
A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tu
A;Reference number: A46519; MUID:93139489; PMID:8423327
A;Accession: B46519
A;Molecule type: protein
A;Residues: 35-62 <PRO>
A;Experimental source: MG-63 osteosarcoma cells
C;Genetics:
A;Gene: GDB:GROI
A;Cross-references: GDB:I20181; OMIM:155730
A;Map position: 4q21-4q21
C;Superfamily: beta-thromboglobulin
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-107/Product: melanoma growth-stimulatory activity #status experimental <MAT>

Query Match 2.4%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
Db 22 LLLLVAA 28
|||||

RESULT 8
149011
gene Ubely protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
A;Reference number: I49011
A;Accession: I49011
R;Chang, B.H.; Li, W.H.
J. Mol. Evol. 40, 70-77, 1995
A;Title: Estimating the intensity of male-driven evolution in rodents by using X-linked
A;Reference number: I49010; MUID:95230700; PMID:7714913
A;Accession: I49011
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-109 <RES>
A;Cross-references: EMBL:U09052; NID:g710299; PIDN:AAC52170.1; PID:g710300

Query Match 2.4%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
Db 22 LLLLVAA 28
|||||

RESULT 9
163169
gene Ubely protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
A;Reference number: I49010; MUID:95230700; PMID:7714913
A;Accession: I63169
R;Chang, B.H.; Li, W.H.
J. Mol. Evol. 40, 70-77, 1995
A;Title: Estimating the intensity of male-driven evolution in rodents by using X-linked
A;Reference number: I49010; MUID:95230700; PMID:7714913
A;Accession: I63169
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-109 <RES>
A;Cross-references: EMBL:U09056; NID:g710305; PIDN:AAC52172.1; PID:g710306
C;Genetics:
A;Gene: Ubely
A;Introns: 14/2; 79/3; 104/3
C;Superfamily: ubiquitin-activating enzyme E1

Query Match 2.4%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TLQLAGT 215
Db 22 TLQLAGT 28
|||||

RESULT 10
B70401
hypothetical protein aq_1176 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
C;Accession: B70401
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70401
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-111 <AQF>
A;Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07206.1; PID:g2983638; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1176
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1176

Query Match 2.4%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 DOVEVEY 236
Db 38 DOVEVEY 44
|||||

RESULT 11
A87594
bleomycin resistance protein [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: A87594
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: A87594
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <STO>
A/Cross-references: GB:AE005673; NID:g13424385; PIDN:AAK24749.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC2785

Query Match 2.4%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 LERGSALT 37
|||||
Db 38 LERGSALT 44

RESULT 12
C81087
hypothetical protein NMB1406 [imported] - Neisseria meningitidis (strain MC58 serogroup
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C/Accession: C81087
R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: C81087
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-120 <TET>
A/Cross-references: GB:AE002489; GB:AE002098; NID:g7226640; PIDN:AAF41769.1; PID:g722664
A/Experimental source: serogroup B, strain MC58
C/Genetics:
A/Gene: NMB1406

Query Match 2.4%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 LPLIFTI 165
|||||
Db 80 LPLIFTI 86

RESULT 13
D82105
conserved hypothetical protein VC2206 [imported] - Vibrio cholerae (strain N16961 serog
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: D82105
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82105

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-145 <HEI>
A/Cross-references: GB:AB004292; GB:AE003852; NID:g9656760; PIDN:AAF95351.1; GSPDB:GN0012
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Map position: 1

Query Match 2.4%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVAA 173
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Db 6 LLLVAA 12

RESULT 14
B44827
FMRamide-like peptide - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C/Accession: B44827
R/Rosoff, M.L.; Burglin, T.R.; Li, C.
J. Neurosci. 12, 2356-2361, 1992
A/Title: Alternatively spliced transcripts of the flp-1 gene encode distinct FMRamide-1
A/Reference number: A44827; MUID:92300457; PMID:1607945
A/Accession: B44827
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-164 <ROS>
A/Note: sequence extracted from NCBI backbone (NCBIP:106594)
C/Keywords: neuropeptide

Query Match 2.4%; Score 7; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVAA 173
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Db 9 LLLVAA 15

RESULT 15
C86241
protein T16B5.9 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: C86241
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:1130712
A/Accession: C86241
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-167 <STO>
A/Cross-references: GB:AE005172; NID:g4874271; PIDN:AAD31336.1; GSPDB:GN00141
C/Genetics:
A/Gene: T16B5.9
A/Map position: 1

Query Match 2.4%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 TSPKAT 221
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Db 55 TSPKAT 61

Search completed: September 16, 2004, 12:57:33
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:40:41 ; Search time 24 Seconds
(without alignments)
629.181 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 230

Sequence: 1 MPLILTYLLFLWLSGYSIAT.....SXLPGRGPBPTEYSTISRP 290

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141661 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.8	107	1 M12A HUMAN	P19875 homo sapien
2	8	2.8	107	1 M12B HUMAN	P19876 homo sapien
3	7	2.4	92	1 SY04 MOUSE	P14097 mus musculus
4	7	2.4	92	1 SY04 RAT	P50230 rattus norv
5	7	2.4	98	1 GROG BOVIN	O46675 bos taurus
6	7	2.4	103	1 GRO SHREP	O46678 ovis aries
7	7	2.4	104	1 GRO2 RABIT	P47854 cryptolagus
8	7	2.4	104	1 GROB BOVIN	O46677 bos taurus
9	7	2.4	107	1 GRO HUMAN	P09341 homo sapien
10	7	2.4	111	1 YB76 AQUAE	O67237 aquifex aeo
11	7	2.4	160	1 LY96 CRIGR	P58755 cricetus
12	7	2.4	171	1 YW87 PSEAE	Q5nyv6 pseudomonas
13	7	2.4	175	1 FARP CABEL	P41855 caenorhabdi
14	7	2.4	185	1 RRF NEIMA	Q9jr52 neisseria m
15	7	2.4	200	1 HA19 MOUSE	P14431 mus musculus
16	7	2.4	255	1 VOIX BACSU	P54535 bacillus su
17	7	2.4	258	1 ETXG STAM	O53382 staphylococ
18	7	2.4	268	1 CS28 PEA	P27490 pisum sativ
19	7	2.4	326	1 HA18 MOUSE	P14430 mus musculus
20	7	2.4	327	1 TAL CHLCV	Q822j3 chlamydophi
21	7	2.4	334	1 VMS1 MOUSE	P14429 mus musculus
22	7	2.4	335	1 HMA5 HPBHE	P13847 heron hepat
23	7	2.4	357	1 DCUP MYCTU	O53231 mycobacteri
24	7	2.4	361	1 QPCT HUMAN	O16769 homo sapien
25	7	2.4	362	1 QPCT DEIRA	Q8rul9 deinococcus
26	7	2.4	397	1 ARGJ THENA	Q9x2a3 t arginine
27	7	2.4	400	1 BJAR MOUSE	P25962 mus musculus
28	7	2.4	400	1 BJAR RAT	P26255 rattus norv
29	7	2.4	425	1 PURA FUSNN	P58793 fusobacteri
30	7	2.4	425	1 PURA FUSUN	O68581 fusobacteri
31	7	2.4	442	1 URAY MOUSE	P12554 mus musculus
32	7	2.4	461	1 TIFI SCHPO	P79065 schizosacch
33	7	2.4	462	1 VATB PYRFU	Q8u4a5 pyrococcus

34	7	2.4	484	1 YLS5 CABEL	P34390 caenorhabdi
35	7	2.4	513	1 CATB PSEAE	Q59635 pseudomonas
36	7	2.4	521	1 VGLC HSPVC	P14378 bovine herp
37	7	2.4	560	1 ASNS CRIGR	P19891 cricetus
38	7	2.4	560	1 ASNS MOUSE	Q61024 mus musculus
39	7	2.4	560	1 ASNS RAT	P45088 rattus norv
40	7	2.4	592	1 SYR COXBU	Q83a98 coxiella bu
41	7	2.4	617	1 ESRI ICTPU	Q9yhz7 ictalurus p
42	7	2.4	622	1 GLMS CORGL	Q8mnd3 c glucosani
43	7	2.4	634	1 SL56 RAT	Q70247 rattus norv
44	7	2.4	635	1 SL56 HUMAN	Q9v289 homo sapien
45	7	2.4	636	1 SL56 RABIT	Q9xt77 cryptolagus
46	7	2.4	694	1 PCK9 MOUSE	Q80w65 mus musculus
47	7	2.4	697	1 SM2A SCHGR	Q9xzcb schistoserc
48	7	2.4	709	1 CN1C HUMAN	Q14123 homo sapien
49	7	2.4	716	1 HEPA HSVEB	P28946 equine herp
50	7	2.4	725	1 AGA1 YEAST	P32323 saccharomyc
51	7	2.4	744	1 REP1 HUMAN	Q96d71 homo sapien
52	7	2.4	813	1 AD33 HUMAN	Q9b211 homo sapien
53	7	2.4	911	1 B3AT HUMAN	P02730 homo sapien
54	7	2.4	968	1 KBF1 HUMAN	P19838 homo sapien
55	7	2.4	971	1 KBF1 MOUSE	P25799 mus musculus
56	7	2.4	1011	1 M3K6 HUMAN	Q95382 homo sapien
57	7	2.4	1047	1 ANPB HUMAN	P20594 homo sapien
58	7	2.4	1065	1 SED4 YEAST	P25365 saccharomyc
59	7	2.4	1087	1 AKA9 RABIT	Q28628 cryptolagus
60	7	2.4	1099	1 CYA7 MOUSE	P51829 mus musculus
61	7	2.4	1159	1 SOR2 MOUSE	Q96pr5 mus musculus
62	7	2.4	1171	1 GLG1 RAT	Q62638 rattus norv
63	7	2.4	1219	1 SOR3 MOUSE	Q8v151 mus musculus
64	7	2.4	1365	1 YAK1 SCHPO	Q09915 schizosacch
65	7	2.4	1400	1 RON HUMAN	Q04912 homo sapien
66	7	2.4	2491	1 MPRI HUMAN	P11717 homo sapien
67	6	2.1	36	1 PSBY ODOSI	P49443 odontella s
68	6	2.1	47	1 YRR7 MYCCA	P43046 mycoplasma
69	6	2.1	54	1 SASG BACPF	P35142 bacillus ps
70	6	2.1	59	1 Y586 PVRAE	Q8zsl3 pyrobaculum
71	6	2.1	64	1 SCX5 ANDMA	P01481 leiurus qui
72	6	2.1	64	1 SCX5 LEIQU	P18679 bacterioph
73	6	2.1	76	1 RCRO BPHKO	P43306 clarias gar
74	6	2.1	86	1 GON2 CLAGA	P73316 synechocyst
75	6	2.1	92	1 RS19 SYN93	P23357 halocarcula
76	6	2.1	99	1 RS10 HALMA	Q09141 bos taurus
77	6	2.1	99	1 SY08 BOVIN	P55000 homo sapien
78	6	2.1	103	1 SLUR HUMAN	P03645 bacterioph
79	6	2.1	103	1 VGS BPST1	Q46676 bos taurus
80	6	2.1	104	1 GROA BOVIN	P43566 saccharomyc
81	6	2.1	106	1 YFD2 YEAST	Q07180 rhodobacter
82	6	2.1	112	1 N1FW RHCCA	Q10500 mycobacteri
83	6	2.1	115	1 ACPM MYCTU	P22228 canine aden
84	6	2.1	117	1 E313 ADECG	Q91kco mus musculus
85	6	2.1	119	1 SY24 MOUSE	P00882 mesocricetu
86	6	2.1	124	1 RNF MESAU	Q9cm90 pasteurella
87	6	2.1	124	1 Y670 PASMU	Q9a6v2 caulobacter
88	6	2.1	127	1 CRGB CAUCR	Q9s2u1 streptomyce
89	6	2.1	128	1 H1S3 STRCO	P75204 mycoplasma
90	6	2.1	128	1 YF75 MYCPN	P24717 cricetus
91	6	2.1	130	1 RNP CRILQ	P24526 mus musculus
92	6	2.1	131	1 MYP2 MOUSE	Q92di5 listeria in
93	6	2.1	137	1 PSIE LISIN	Q8y8g9 listeria mo
94	6	2.1	137	1 PSIE LISMO	Q9xt91 macropus eu
95	6	2.1	139	1 IL5 MACEU	Q58157 methanococ
96	6	2.1	147	1 HEMT METJA	P14830 lycopersico
97	6	2.1	151	1 SOD1 LYCES	Q43779 lycopersico
98	6	2.1	151	1 SOD2 LYCES	P52490 saccharomyc
99	6	2.1	153	1 UBCC YEAST	P48923 candida par
100	6	2.1	153	1 NU6M CANPA	P52490 saccharomyc
101	6	2.1	156	1 RS7 STRCO	Q910x4 streptomyce
102	6	2.1	156	1 RS7 STRRP	P95847 streptomyce
103	6	2.1	156	1 Y003 METJA	Q60313 methanococ
104	6	2.1	160	1 YVYG BACSU	P39808 bacillus su
105	6	2.1	163	1 ILVH ECOLI	P00894 escherichia
106	6	2.1	163	1 ILVH SALTY	P21622 salmonella

107	6	2.1	170	1	ARGR MYCTU	P49992 mycobacteri	180	2.1	274	1	YX1_CVHSA	P59632 human coron
108	6	2.1	171	1	CX5 NEUCR	P06810 neurospora	181	2.1	275	1	YMA3_CABEL	P34454 caenorhabdi
109	6	2.1	171	1	Y762_ARCFU	O29496 archaeoglob	182	2.1	280	1	PANB_MYCVN	Q917b2 mycobacteri
110	6	2.1	171	1	YCX7_YEAST	P26652 saccharomyc	183	2.1	281	1	PANB_MYCTU	Q10505 mycobacteri
111	6	2.1	173	1	PYR3_STREF3	Q8K7Y5 streptococc	184	2.1	283	1	VNS4_MSTV	P33521 maize strip
112	6	2.1	173	1	PYR3_STREF8	P59013 streptococc	185	2.1	284	1	DRN1_MOUSE	P49183 mus musculu
113	6	2.1	173	1	PYR3_STREFY	Q9a0d0 streptococc	186	2.1	285	1	DDH2_HUMAN	O95865 homo sapien
114	6	2.1	187	1	VGG_BPALK3	P12811 bacterioph	187	2.1	286	1	PANB_MYCLE	Q9fnd5 arabidopsi
115	6	2.1	187	1	VGG_BPCHK	Q38042 bacterioph	188	2.1	286	1	UDU1_ARATH	Q9fnd5 arabidopsi
116	6	2.1	188	1	C56T_ECOLI	P75925 escherichia	189	2.1	286	1	VNS4_RSVT	P34961 rice stripe
117	6	2.1	192	1	LUM_EBIT	O46379 oryctolagus	190	2.1	286	1	VNS4_BSVT	Q00847 rice stripe
118	6	2.1	192	1	Y54I_PSESM	Q8a56 pseudomonas	191	2.1	289	1	BSN1_BACSU	Q03091 bacillus su
119	6	2.1	193	1	H5_CARMO	P06513 calina mos	192	2.1	289	1	QCRC_MYCLE	P69583 mycobacteri
120	6	2.1	193	1	MOBA_RHOSH	P95645 rhodobacter	193	2.1	289	1	U714_HUMAN	P50876 homo sapien
121	6	2.1	197	1	T485_HUMAN	O14894 homo sapien	194	2.1	292	1	U714_MOUSE	Q925f3 mus musculu
122	6	2.1	197	1	VR26_NPVOP	O10276 orgyia pseu	195	2.1	294	1	CAMG_MOUSE	P49070 mus musculu
123	6	2.1	198	1	YCX1_PORPU	P51354 porphyra pu	196	2.1	296	1	CAMG_HUMAN	P49069 homo sapien
124	6	2.1	200	1	YCF4_LOTJA	Q9bbr3 lotus japon	197	2.1	299	1	CRX_BOVIN	Q9xsk0 bos taurus
125	6	2.1	202	1	SODP_FEA	P11964 pisum sativ	198	2.1	299	1	CRX_HUMAN	O43186 homo sapien
126	6	2.1	202	1	WR59_ARATH	Q9s109 arabidopsi	199	2.1	299	1	CRX_MOUSE	O54751 mus musculu
127	6	2.1	206	1	YQ11_BACSU	P54525 bacillus su	200	2.1	301	1	CTF5_HUMAN	Q9uja2 homo sapien
128	6	2.1	208	1	YM16_YEAST	P40206 saccharomyc	201	2.1	303	1	CD38_RAT	Q64244 rattus norv
129	6	2.1	211	1	MOTX_VIBPA	P40608 vibrio para	202	2.1	303	1	CTF5_MOUSE	Q80zm8 mus musculu
130	6	2.1	211	1	SODP_ORVSA	P93407 oryza sativ	203	2.1	305	1	GSPC_VIBCH	P45777 vibrio chol
131	6	2.1	212	1	ATP6_TROHI	O03570 tropidurus	204	2.1	306	1	PRVA_ANASP	Q8yvt3 anabaena sp
132	6	2.1	212	1	ATP6_TROMO	O03359 tropidurus	205	2.1	306	1	YLIC_ECOLI	P75798 escherichia
133	6	2.1	214	1	Y330_STR3	P59254 streptococc	206	2.1	308	1	Y04P_MYCTU	Q10786 mycobacteri
134	6	2.1	214	1	DSBA_PSESM	O52376 pseudomonas	207	2.1	309	1	YQGH_BACSU	P46339 bacillus su
135	6	2.1	215	1	O2A6_HUMAN	Q96r47 homo sapien	208	2.1	311	1	FMT_STRPN	Q97pa6 streptococc
136	6	2.1	216	1	E325_ADECC	Q69599 canine aden	209	2.1	311	1	FMT_STRPN6	Q8dnr7 streptococc
137	6	2.1	216	1	SODP_ARATH	O78310 arabidopsi	210	2.1	311	1	YCAV_CLOXL	P38943 clostridium
138	6	2.1	216	1	SODP_ZANAE	O65175 zantedeschi	211	2.1	311	1	DHEX_ANAPL	O57314 anas platyr
139	6	2.1	217	1	ORAS_HUMAN	Q96r48 homo sapien	212	2.1	313	1	PYRB_RHIME	Q92ql5 rhizobium m
140	6	2.1	217	1	SODP_LYCS	P14831 lycopersico	213	2.1	314	1	MER2_YEAST	F21651 saccharomyc
141	6	2.1	220	1	SODP_SOLCS	O04997 solidago ca	214	2.1	314	1	YP69_MYCTU	Q50652 mycobacteri
142	6	2.1	220	1	VM02_VACC	P21092 vaccinia vi	215	2.1	315	1	O3A2_HUMAN	P47893 homo sapien
143	6	2.1	221	1	NUSB_SYNY3	P74393 synecocyst	216	2.1	318	1	MYOD_RAT	Q02346 rattus norv
144	6	2.1	221	1	TVSY_METH	Q26868 methanobact	217	2.1	318	1	Y391_BUCBP	O89ac3 buchnera ap
145	6	2.1	222	1	SODP_SPIOL	P07505 spinacia ol	218	2.1	319	1	CJ06_HUMAN	P51203 porphyra pu
146	6	2.1	222	1	TVSY_METIM	P80305 methanobact	219	2.1	320	1	YCS5_FORPU	P51203 porphyra pu
147	6	2.1	226	1	GSFB_AERHY	P45755 aeromonas h	220	2.1	322	1	FSM_BRARE	Q99yv4 brachydanio
148	6	2.1	229	1	CEMA_ATRBE	Q8s8w5 atropa bell	221	2.1	322	1	HBM3_CAUCR	Q9abz8 caulobacter
149	6	2.1	229	1	CEMA_LOTJA	P58155 lotus japon	222	2.1	327	1	OPT_CANFA	P83286 canis fami
150	6	2.1	229	1	CEMA_SOYBN	P49160 glycine max	223	2.1	330	1	PRC2_FORGI	P33437 porphyromon
151	6	2.1	229	1	CEMA_TOBAC	P12213 nicotiana t	224	2.1	331	1	LDHC_HUMAN	P07864 homo sapien
152	6	2.1	230	1	YGTQ_ECOLI	P42598 escherichia	225	2.1	334	1	PRC1_FORGI	P59916 porphyromon
153	6	2.1	231	1	FCAT_FSEFU	Q01103 pseudomonas	226	2.1	335	1	DUSA_SHEON	Q8aaj0 shewanella
154	6	2.1	231	1	Y236_CAMJE	Q9p1q8 campylobact	227	2.1	335	1	ZDH1_STAAM	Q99s81 staphylococ
155	6	2.1	235	1	HG12_CABEL	Q09390 caenorhabdi	228	2.1	335	1	ZDH1_STAAM	Q8nvd1 staphylococ
156	6	2.1	236	1	COAT_CMV	P11642 maize chlor	229	2.1	336	1	NOSO_BACSU	O34453 bacillus su
157	6	2.1	236	1	STX8_HUMAN	Q9unk0 homo sapien	230	2.1	336	1	ZDH1_STAEP	Q8grj7 staphylococ
158	6	2.1	236	1	STX8_RAT	Q9z2q7 rattus norv	231	2.1	337	1	CMST_HUMAN	P78382 homo sapien
159	6	2.1	237	1	ATP6_PETWA	Q35538 petromyzon	232	2.1	337	1	GCP_SALTY	P40731 salmonella
160	6	2.1	239	1	TFB8_MOUSE	P29972 mus musculu	233	2.1	337	1	GPDA_FASWT	Q9cl17 pasteurella
161	6	2.1	241	1	GLTL_ECOLI	P41076 escherichia	234	2.1	337	1	2B65_HUMAN	Q95218 homo sapien
162	6	2.1	242	1	CRP4_LIMPO	P06206 limulus pol	235	2.1	338	1	FOSB_MOUSE	P13346 mus musculu
163	6	2.1	243	1	TLP1_CASSA	Q9smh2 castanea sa	236	2.1	338	1	LUM_HUMAN	P51884 homo sapien
164	6	2.1	243	1	ZIPA_XANAC	Q8m10 xanthomonas	237	2.1	338	1	LUM_MOUSE	P51885 mus musculu
165	6	2.1	244	1	FNPA_PSEST	P47200 pseudomonas	238	2.1	338	1	LUM_RAT	P51886 rattus norv
166	6	2.1	244	1	ZIPA_XANCP	Q9pab7 xanthomonas	239	2.1	338	1	YEF6_YEAST	P40093 saccharomyc
167	6	2.1	246	1	ATP6_CANPA	Q3671 candida par	240	2.1	340	1	AAZB_CHICK	O13076 gallus gall
168	6	2.1	248	1	1433_CABEL	P41932 caenorhabdi	241	2.1	340	1	ILVE_HELPY	Q9xjfi helicobacte
169	6	2.1	252	1	TI13_ARATH	O82598 arabidopsi	242	2.1	340	1	ILVE_HELPY	O26004 helicobacte
170	6	2.1	258	1	KDSB_PASMU	P57883 pasteurella	243	2.1	340	1	YK4F_CABEL	O17606 caenorhabdi
171	6	2.1	259	1	RNS2_ARATH	P42814 arabidopsi	244	2.1	341	1	TA2R_RAT	P34978 rattus norv
172	6	2.1	265	1	MPH1_HOLIA	P43216 holcus lana	245	2.1	342	1	LUM_BOVIN	Q05443 bos taurus
173	6	2.1	266	1	YM42_CLOPE	Q9xi79 clostridium	246	2.1	343	1	TA2R_CERAB	P56486 cercopithe
174	6	2.1	267	1	DEMI_YEAST	P14020 saccharomyc	247	2.1	344	1	HYGH_HYONI	P24397 hyoscymus
175	6	2.1	268	1	CEBD_MOUSE	Q00322 mus musculu	248	2.1	345	1	TRPD_AERPE	Q9y8t2 aeropyrum p
176	6	2.1	268	1	CEBD_RAT	Q03484 rattus norv	249	2.1	348	1	CTH2_MOUSE	Q9cyc5 mus musculu
177	6	2.1	269	1	YFCA_ECOLI	P14008 escherichia	250	2.1	350	1	GANA_ASPAC	P48842 aspergillus
178	6	2.1	274	1	CB2B_PINSY	P5194 pinus sylve	251	2.1	351	1	B3AR_CAVPO	Q60483 cavia porce
179	6	2.1	274	1	YB03_MYCTU	P71671 mycobacteri	252	2.1	353	1	CCPA_ACEXY	P37697 acetobacter

253	6	2.1	353	1	CV04_MOUSE	Q8r5a6 mus musculus	326	6	2.1	422	1	GAS7_RAT	O55148 rattus norv
254	6	2.1	353	1	TCPH_TETTH	P54410 tetrahymena	327	6	2.1	422	1	GSA_CHLTR	O84212 chlamydia t
255	6	2.1	355	1	TRPD_AZOBH	P26924 azospirillum	328	6	2.1	424	1	HEMI_CHLVI	P28462 chlorobium
256	6	2.1	356	1	MURG_YERPE	Q8zie9 versinia pe	329	6	2.1	424	1	MSI3_ARATH	O22469 arabidopsis
257	6	2.1	356	1	SECV_BUCKA	P49976 buchnera ap	330	6	2.1	425	1	IRIS_MOUSE	Q08619 mus musculus
258	6	2.1	357	1	CADH_FOFDE	P31657 populus del	331	6	2.1	425	1	PAR1_HUMAN	P25116 homo sapien
259	6	2.1	358	1	ILVE_STAAM	Q99w55 staphylococ	332	6	2.1	425	1	PAR1_FAPHA	F78488 papio namad
260	6	2.1	358	1	ILVE_STAEP	Q8c978 staphylococ	333	6	2.1	426	1	HEMI_RHOBA	Q7ukz2 rhodospirell
261	6	2.1	360	1	CVS2_MAIZE	Q10717 zea mays (m	334	6	2.1	428	1	UL61_CRILLO	Q00991 cricetus
262	6	2.1	360	1	ELV2_MOUSE	Q60899 mus musculus	335	6	2.1	431	1	UL61_HCMVA	P16818 human cytom
263	6	2.1	360	1	YOFA_CABEL	Q09337 caenorhabdi	336	6	2.1	433	1	QADB_KLEPN	P13156 klebsiella
264	6	2.1	361	1	OPCT_BOVIN	Q82120 bos taurus	337	6	2.1	433	1	QADB_SALTI	Q829m6 salmonella
265	6	2.1	362	1	ILVE_STRGO	Q86505 streptomyce	338	6	2.1	435	1	QADB_HAEDU	Q9if98 haemophilus
266	6	2.1	364	1	FTSW_BORBU	Q44775 borrelia bu	339	6	2.1	436	1	SH6_RAT	P31388 rattus norv
267	6	2.1	364	1	UFTG_PEA	O04300 pisum sativ	340	6	2.1	436	1	MUAI_BACSU	P70965 bacillus su
268	6	2.1	365	1	BCSA_BACSU	P54157 bacillus su	341	6	2.1	438	1	MUAI_LACPL	Q88u5 lactobacill
269	6	2.1	365	1	MAP3_SCHPO	P31397 schizosacch	342	6	2.1	438	1	PROA_ANASP	Q8yv15 anabaena sp
270	6	2.1	368	1	ILVE_MYCLE	Q32954 mycobacteri	343	6	2.1	440	1	SH6_HUMAN	P50406 homo sapien
271	6	2.1	368	1	ILVE_MYCTU	Q10339 mycobacteri	344	6	2.1	440	1	SH6_MOUSE	Q9rlc8 mus musculus
272	6	2.1	369	1	TAZR_HUMAN	P21731 homo sapien	345	6	2.1	441	1	DCTA_RHIME	P20672 rhizobium m
273	6	2.1	372	1	AROB_PROMM	Q7v781 prochloroco	346	6	2.1	442	1	DTA2_RHILO	Q986r8 rhizobium l
274	6	2.1	372	1	SL17B_HUMAN	Q94768 homo sapien	347	6	2.1	443	1	YAEI_HAEIN	P44936 haemophilus
275	6	2.1	373	1	MLE_TRICU	P46057 trichosporo	348	6	2.1	444	1	DCTA_RHILE	Q01857 rhizobium l
276	6	2.1	375	1	MYG1_HUMAN	Q9hb07 homo sapien	349	6	2.1	444	1	LH2A_MOUSE	Q99kc8 mus musculus
277	6	2.1	376	1	NIFV_AZOBH	P70728 azospirillu	350	6	2.1	445	1	EM47_YEAST	P43555 saccharomyc
278	6	2.1	376	1	NIFV2_ANASP	P58637 anabaena sp	351	6	2.1	445	1	MESJ_BUCAP	Q8ka23 buchnera ap
279	6	2.1	377	1	NORW_SALTI	Q82484 salmonella	352	6	2.1	446	1	GRWD_HUMAN	Q9bq67 homo sapien
280	6	2.1	377	1	NORW_SALTY	Q8zmj6 salmonella	353	6	2.1	448	1	DCTA_AGRYS	P58734 agrobacteri
281	6	2.1	377	1	PEPC_MACFU	P03955 macaca fusc	354	6	2.1	451	1	NORM_DEIRA	Q9ry44 deinococcus
282	6	2.1	380	1	MYG1_MOUSE	Q9jk81 mus musculus	355	6	2.1	454	1	VNUC_THOYG	P89216 thogoto vir
283	6	2.1	381	1	E2BB_YEAST	P32502 saccharomyc	356	6	2.1	458	1	C6ST_CHICK	Q92179 gallus gall
284	6	2.1	381	1	PPAP_RAT	P20646 rattus norv	357	6	2.1	460	1	LE12_SULTO	Q971s5 sulfolobus
285	6	2.1	381	1	SSUD_PSEAE	Q9hy32 pseudomonas	358	6	2.1	461	1	DCTA_RHIGA	Q947k6 rhizobium g
286	6	2.1	382	1	NIFV_AZOBH	P23122 azotobacter	359	6	2.1	463	1	RLB3_HYDMR	Q59462 hydrogenovi
287	6	2.1	382	1	SSUD_BUTSP	Q9khr3 butiauxell	360	6	2.1	465	1	TPSN_MOUSE	Q9r233 mus musculus
288	6	2.1	382	1	SSUD_PSEPK	Q88r95 pseudomonas	361	6	2.1	465	1	VATB_PYRAB	Q9uxu8 pyrococcus
289	6	2.1	382	1	SSUD_PSEPU	Q85764 pseudomonas	362	6	2.1	465	1	VATB_PYRHO	O57729 pyrococcus
290	6	2.1	382	1	SSUD_PSESP	Q9khs2 pseudomonas	363	6	2.1	470	1	PROP_CAVPO	Q64181 cavia porce
291	6	2.1	382	1	SSUD_YERPE	Q8zb04 versinia pe	364	6	2.1	471	1	ATPA_PROMO	P29706 propionigen
292	6	2.1	384	1	OXAA_SYNOI	P74155 synectocyst	365	6	2.1	473	1	SYC_METMA	Q8byq1 methanosarc
293	6	2.1	385	1	NIFV_AZOV1	P05342 azotobacter	366	6	2.1	475	1	SYC_CHLMU	Q9ple0 chlamydia m
294	6	2.1	387	1	COAT_TB5VB	P11795 tomato bush	367	6	2.1	477	1	DTA1_RHILO	Q98av2 rhizobium l
295	6	2.1	388	1	PEPC_CALJA	Q9n2d3 callithrix	368	6	2.1	477	1	P3_HUMAN	P09131 homo sapien
296	6	2.1	388	1	PEPC_HUMAN	P20142 homo sapien	369	6	2.1	479	1	B3GP_DROME	Q9vctg7 drosophila
297	6	2.1	388	1	TEA6_BURCE	P24575 burkholderi	370	6	2.1	479	1	GLYC_NEUCR	P34898 neurospora
298	6	2.1	388	1	YF02_AQUAE	O67472 aquifex aeo	371	6	2.1	483	1	PREG_NEUCR	Q06712 neurospora
299	6	2.1	389	1	GSPL_AERHY	P45789 aeromonas h	372	6	2.1	485	1	ALGI_PSEPK	Q88nd2 pseudomonas
300	6	2.1	390	1	ISDF_BRUME	Q8yhd8 b ispd/ispf	373	6	2.1	485	1	GATA_CLOTE	Q89111 clostridium
301	6	2.1	390	1	ISDF_BRUSU	Q8g0h4 b ispd/ispf	374	6	2.1	485	1	NOE1_HUMAN	Q99784 mus sapien
302	6	2.1	390	1	NCF1_HUMAN	P14598 homo sapien	375	6	2.1	485	1	NOE1_MOUSE	O88998 mus musculus
303	6	2.1	390	1	SUCC_COXBU	P53592 coxiella bu	376	6	2.1	485	1	NOE1_RAT	Q62609 rattus norv
304	6	2.1	392	1	CMLR_STRLI	P31141 streptomyce	377	6	2.1	485	1	PODX_RAT	Q9wtq2 rattus norv
305	6	2.1	392	1	MP14_ABEAR	P28744 ambrosia ar	378	6	2.1	487	1	HEP_DROME	Q23977 drosophila
306	6	2.1	396	1	HEMI_CLOBAB	Q97mu6 clostridium	379	6	2.1	488	1	ZDHE_HUMAN	Q81zn3 homo sapien
307	6	2.1	400	1	HLFK_VIBPA	P40605 vibrio para	380	6	2.1	490	1	C71L_ARATH	Q98t12 arabidopsis
308	6	2.1	403	1	GBAB_DICDI	P34046 dictyosteli	381	6	2.1	490	1	C71M_ARATH	Q9at11 arabidopsis
309	6	2.1	404	1	NEED_PINRA	O04407 pinus radia	382	6	2.1	490	1	C72F_ARATH	Q91w27 arabidopsis
310	6	2.1	408	1	YL12_PYRAE	Q8zvu9 pyrobaculum	383	6	2.1	490	1	ENGA_CHLMU	Q9ylm3 chlamydia m
311	6	2.1	409	1	CP52_STRCC	Q59831 streptomyce	384	6	2.1	490	1	ENGA_CHLTR	O84709 chlamydia t
312	6	2.1	411	1	LCYB_SYNP7	Q55276 synectococc	385	6	2.1	494	1	CPA4_MOUSE	P15392 mus musculus
313	6	2.1	414	1	PIT_MYCLE	Q50173 mycobacteri	386	6	2.1	494	1	CPA5_MOUSE	P20852 mus musculus
314	6	2.1	414	1	SYC2_MYCTU	Q33264 mycobacteri	387	6	2.1	494	1	HEX3_ADEMI	O10408 mouse adeco
315	6	2.1	414	1	YOJL_BACSU	P18152 bacillus su	388	6	2.1	496	1	DHAL_CLAHE	P40108 cladosporiu
316	6	2.1	416	1	METK_SYNEL	Q8dk88 synectococc	389	6	2.1	497	1	CV04_MACEA	Q95k11 macaca fasc
317	6	2.1	417	1	IF_MOUSE	P52787 mus musculus	390	6	2.1	497	1	GALT_ENTFA	Q836n8 enterococcu
318	6	2.1	419	1	PNK2_CABEL	Q8mx14 caenorhabdi	391	6	2.1	497	1	HMES_DROME	P18488 drosophila
319	6	2.1	421	1	GAS7_MOUSE	Q80780 mus musculus	392	6	2.1	497	1	IRF5_MOUSE	P56477 mus musculus
320	6	2.1	421	1	SP39_BRUAB	Q06875 brucella ab	393	6	2.1	498	1	IYEN_BCOLI	P31473 escherichia
321	6	2.1	421	1	SP39_BRUME	Q8yce2 brucella me	394	6	2.1	499	1	MATK_CERME	Q8mey4 ceratozamia
322	6	2.1	421	1	SP39_BRUSU	Q8fvx5 brucella su	395	6	2.1	499	1	WETA_PENCH	Q01870 penicillium
323	6	2.1	421	1	SVTC_HUMAN	Q81v01 homo sapien	396	6	2.1	500	1	C72W_ARATH	Q91lp5 arabidopsis
324	6	2.1	421	1	SVTC_MOUSE	Q920n7 mus musculus	397	6	2.1	502	1	ACH7_CHICK	P22770 gallus gall
325	6	2.1	421	1	SVTC_RAT	P97610 rattus norv	398	6	2.1	502	1	ACH7_HUMAN	P36544 homo sapien

399	6	2.1	502	1	SYK_HAEIN	P43825 haemophilus	472	6	2.1	624	1	P212_HUMAN	Q9nmz6 homo sapien
400	6	2.1	502	1	Y2R2_AGRVI	P70795 agrobacteri	473	6	2.1	625	1	FANA_HELAS	Q25011 helix asper
401	6	2.1	503	1	PODX_MOUSE	Q9r0m4 mus musculu	474	6	2.1	626	1	EXON_HSV11	P04294 herpes simp
402	6	2.1	503	1	SYE_CHLTE	Q5f724 chlorobium	475	6	2.1	626	1	HCYB_SURCA	Q9nfh9 eurypalma c
403	6	2.1	504	1	PUPP_HAEIN	P45174 haemophilus	476	6	2.1	626	1	PRIM_LISIN	Q92bq5 listeria in
404	6	2.1	504	1	YBLH_SCHPO	Q10341 schizosacch	477	6	2.1	626	1	THIC_PSEPK	Q88da5 pseudomonas
405	6	2.1	506	1	ALG6_SCHPO	Q43053 schizosacch	478	6	2.1	627	1	Z264_HUMAN	Q82996 homo sapien
406	6	2.1	506	1	C992_ARATH	Q42602 arabidopsis	479	6	2.1	631	1	IL16_PANTR	O62666 pan troglod
407	6	2.1	508	1	CG12_HUMAN	Q96kn2 homo sapien	480	6	2.1	638	1	YCSB_SCHPO	O74910 schizosacch
408	6	2.1	511	1	INO1_PHAVU	Q41107 phaseolus v	481	6	2.1	639	1	KNG_RAT	P08934 rattus norv
409	6	2.1	516	1	OXLA_CROAD	Q93364 crotalus ad	482	6	2.1	640	1	DXS_CAUCR	Q9a6m5 caulobacter
410	6	2.1	516	1	YLAB_ECOLI	P77473 escherichia	483	6	2.1	640	1	IFI4_MOUSE	P15092 mus musculu
411	6	2.1	517	1	CPN1_RANCA	Q92104 rana catesb	484	6	2.1	645	1	SUBB_BACSU	P16396 bacillus su
412	6	2.1	517	1	COV4_HUMAN	Q8wu47 homo sapien	485	6	2.1	645	1	Y081_CABEL	P34617 caenorhabdi
413	6	2.1	521	1	COAT_BPT4	P04535 bacterioph	486	6	2.1	647	1	PARE_STRPN	Q59961 streptococc
414	6	2.1	524	1	G6PD_SYNP7	P29686 synchococc	487	6	2.1	652	1	NAK1_SCHPO	O75011 schizosacch
415	6	2.1	524	1	Y233_SYNY3	P74217 synechoyast	488	6	2.1	657	1	CTPD_MYCTU	O53160 mycobacteri
416	6	2.1	526	1	F2P2_MOUSE	P10852 mus musculu	489	6	2.1	670	1	AC11_NEUCR	O8x097 neurospora
417	6	2.1	527	1	TCPD_SCHPO	P50999 schizosacch	490	6	2.1	673	1	Z145_HUMAN	O05516 homo sapien
418	6	2.1	528	1	PODX_HUMAN	Q00592 homo sapien	491	6	2.1	679	1	NADE_MYCTE	P71911 mycobacteri
419	6	2.1	528	1	WR42_ARATH	Q9xec3 arabidopsis	492	6	2.1	680	1	NADE_MYCTE	Q9cbz6 mycobacteri
420	6	2.1	529	1	Y4P2_HUMAN	P08195 homo sapien	493	6	2.1	685	1	DL14_HUMAN	Q0nr61 homo sapien
421	6	2.1	529	1	Y777_MYCTU	O50644 mycobacteri	494	6	2.1	687	1	VIUA_VIBCH	Q00964 vibrio chol
422	6	2.1	532	1	YOAD_ECOLI	P76261 escherichia	495	6	2.1	699	1	EPG_AQUAE	O66428 aquifex aeo
423	6	2.1	533	1	YX03_MYCTU	Q50722 mycobacteri	496	6	2.1	699	1	EPG_AQUAE	P46211 aquifex pyr
424	6	2.1	535	1	YVRG_CLOAB	Q97161 clostridium	497	6	2.1	702	1	OPGB_XANCP	O8pdd7 xanthomonas
425	6	2.1	536	1	OXAA_WOLSU	P60037 wolinnella s	498	6	2.1	703	1	CNAT_MOUSE	Q8bmd6 mus musculu
426	6	2.1	537	1	PVRG_RICCN	Q92197 rickettsia	499	6	2.1	705	1	CANX_CHICK	P00789 gallus gall
427	6	2.1	537	1	TVR1_YEAST	P07147 mus musculu	500	6	2.1	705	1	MMLC_STRCO	O88022 streptomyce
428	6	2.1	538	1	GLE1_YEAST	Q12315 saccharomyc	501	6	2.1	705	1	MMLC_STRCO	Q9xa86 streptomyce
429	6	2.1	538	1	WR31_ARATH	Q93w70 arabidopsis	502	6	2.1	705	1	YFP9_CAEEL	P34562 caenorhabdi
430	6	2.1	540	1	OXAA_WIGBR	Q9d318 wiggleswort	503	6	2.1	706	1	EPG_LBPIN	O8f983 leptospira
431	6	2.1	544	1	OXAA_BORBU	O51398 borrelia bu	504	6	2.1	707	1	CNAT_HUMAN	Q9np78 homo sapien
432	6	2.1	545	1	MTR9_MOUSE	Q922d0 mus musculu	505	6	2.1	710	1	NECB_HYDAT	P29145 hydra atten
433	6	2.1	546	1	PHR2_CANAL	Q13318 candida alb	506	6	2.1	711	1	LXE3_HUMAN	Q9byj1 homo sapien
434	6	2.1	548	1	CH60_EHREI	P48214 ehrlichia r	507	6	2.1	711	1	LXE3_MOUSE	Q9wv07 mus musculu
435	6	2.1	548	1	CH60_EHREI	Q32606 ehrlichia s	508	6	2.1	713	1	CAN1_MOUSE	O35350 mus musculu
436	6	2.1	549	1	MTR9_HUMAN	Q96qg7 homo sapien	509	6	2.1	713	1	CAN1_RAT	P97571 rattus norv
437	6	2.1	551	1	CC14_YEAST	Q0684 saccharomyc	510	6	2.1	713	1	PRML_BRARE	Q9w757 brachydanio
438	6	2.1	551	1	L1DP_EC016	Q9xd59 escherichia	511	6	2.1	713	1	YXK1_YEAST	P50944 saccharomyc
439	6	2.1	551	1	L1DP_EC01	P33231 escherichia	512	6	2.1	714	1	CAN1_HUMAN	P50944 saccharomyc
440	6	2.1	551	1	PODX_RABIT	Q28645 cryetolagus	513	6	2.1	714	1	CAN1_MACFA	Q9glg2 macaca fasc
441	6	2.1	552	1	HAS2_CHICK	O57424 gallus gall	514	6	2.1	714	1	CAN1_PIG	P35750 sus scrofa
442	6	2.1	552	1	YQ92_METJA	Q58688 methanococc	515	6	2.1	722	1	FLID_TREPA	O83842 treponema p
443	6	2.1	555	1	ALG9_YEAST	P53868 saccharomyc	516	6	2.1	725	1	CTPC_MYCLE	Q9gcl1 mycobacteri
444	6	2.1	557	1	HYB_SERMA	P53321 serratia ma	517	6	2.1	726	1	RNR_MYCPN	P75529 mycoplasma
445	6	2.1	558	1	TCPH_TETPY	P54409 tetrahymena	518	6	2.1	728	1	MYBA_XENLA	Q05935 xenopus lae
446	6	2.1	560	1	YDEN_ECOLI	P77318 escherichia	519	6	2.1	739	1	PO21_CHICK	P15143 gallus gall
447	6	2.1	563	1	MDL1_PRUSE	P52706 prunus sero	520	6	2.1	741	1	RNSA_HUMAN	Q05823 homo sapien
448	6	2.1	566	1	MXID_SHIFL	Q04641 shigella fl	521	6	2.1	741	1	TKTC_SOLTU	Q43848 solanum tub
449	6	2.1	566	1	MXID_SHISO	Q55293 shigella so	522	6	2.1	743	1	PO21_HUMAN	P14859 homo sapien
450	6	2.1	570	1	FLIF_HHOSH	Q53151 rhodobacter	523	6	2.1	744	1	HXC1_HAEIN	P44523 haemophilus
451	6	2.1	573	1	MDL3_PRUSE	P52707 prunus sero	524	6	2.1	745	1	PO21_PIG	Q29076 sus scrofa
452	6	2.1	574	1	GAGJ_DROFU	P13131 drosophila	525	6	2.1	747	1	ORPB_HUMAN	Q9bxb4 homo sapien
453	6	2.1	575	1	UL87_EBV	P25215 Epstein-bar	526	6	2.1	749	1	CATA_LEGPN	Q9wxb9 legionella
454	6	2.1	577	1	YGSU_YEAST	P53333 saccharomyc	527	6	2.1	753	1	YP6A_CAEEL	Q09219 caenorhabdi
455	6	2.1	580	1	CVRA_PSEBM	Q87vb6 pseudomonas	528	6	2.1	758	1	PARC_RHIME	Q59749 rhizobium m
456	6	2.1	580	1	PRPX_BACCE	Q81cb2 bacillus ce	529	6	2.1	759	1	PURL_CHLTE	Q8kd17 chlorobium
457	6	2.1	581	1	YH2_YEAST	P38767 saccharomyc	530	6	2.1	760	1	PO21_XENLA	P16143 xenopus lae
458	6	2.1	583	1	TREA_HUMAN	Q43280 homo sapien	531	6	2.1	763	1	GLH1_CAEEL	P34689 caenorhabdi
459	6	2.1	593	1	SUNT_YEAST	P36150 saccharomyc	532	6	2.1	770	1	PO21_MOUSE	P25425 mus musculu
460	6	2.1	594	1	DCP2_SCHPO	Q92345 schizosacch	533	6	2.1	775	1	POQF_PSEAE	Q912d2 pseudomonas
461	6	2.1	601	1	KEFB_SALTI	Q821y7 salmonella	534	6	2.1	777	1	RTN1_RAT	Q64548 rattus norv
462	6	2.1	601	1	KEFB_SALTY	Q821l3 salmonella	535	6	2.1	780	1	A4_TETFL	O73683 tetraodon f
463	6	2.1	606	1	T9S1_HUMAN	Q15321 homo sapien	536	6	2.1	781	1	YKGT_CAEEL	P46557 caenorhabdi
464	6	2.1	606	1	T9S1_MOUSE	Q9dbu0 mus musculu	537	6	2.1	788	1	PUR2_YARLI	Q99148 y bifunctio
465	6	2.1	608	1	GLMS_BUCAI	P57138 b glucosami	538	6	2.1	790	1	SEIL_MOUSE	Q92966 mus musculu
466	6	2.1	609	1	FRI_ARATH	Q9fdw0 arabidopsis	539	6	2.1	793	1	NECA_HYDAT	P25146 hydra atten
467	6	2.1	616	1	YKA4_CAEEL	P34256 caenorhabdi	540	6	2.1	805	1	SUS1_SOLTU	P10691 solanum tub
468	6	2.1	620	1	DNAA_PORPU	P30723 porphyra pu	541	6	2.1	805	1	SUS2_SOLTU	P49039 solanum tub
469	6	2.1	620	1	UL32_HSVBB	P28952 equine herp	542	6	2.1	805	1	SUSY_LYCES	P49037 lycopersico
470	6	2.1	622	1	CN31_HUMAN	Q96ne9 homo sapien	543	6	2.1	808	1	DHG_GLUOX	P27175 glyconobact
471	6	2.1	623	1	ZPI_MOUSE	Q20005 mus musculu	544	6	2.1	809	1	AL14_SCHPO	O94534 schizosacch

545	6	2.1	816	1	NP2A_MOUSE	P97450	618	1	ITA5_MOUSE	P11688	mus musculus
546	6	2.1	822	1	YJF1_YEAST	P47046	619	1	PDR1_YEAST	P1383	saccharomyc
547	6	2.1	824	1	NSF_CAEEL	P94392	620	1	ISK5_HUMAN	P9438	homo sapien
548	6	2.1	824	1	CADH_MOUSE	Q9r100	621	1	EXBC_MYCLE	Q9cd47	mycobacteri
549	6	2.1	827	1	CADH_RAT	P55281	622	1	HSR_HUMAN	P25092	homo sapien
550	6	2.1	827	1	GYRA_HELPY	P48370	623	1	CYA7_HUMAN	P51828	homo sapien
551	6	2.1	828	1	GYRA_HELPJ	Q9z1d9	624	1	AT18_HUMAN	Q8te60	homo sapien
552	6	2.1	831	1	TVID_SALTI	Q04974	625	1	BUD2_YEAST	P33314	saccharomyc
553	6	2.1	836	1	RPOC_CHLVU	P56300	626	1	BUD2_YEAST	P33080	saccharomyc
554	6	2.1	837	1	AT54_HUMAN	Q75173	627	1	KBQ9_YEAST	O73791	brachydanio
555	6	2.1	844	1	PAC_KLUCI	P07941	628	1	TIE2_BRARE	P37144	saccharomyc
556	6	2.1	846	1	PAC_ECOLI	P06875	629	1	YB95_YEAST	P38111	saccharomyc
557	6	2.1	848	1	AMPN_LACLA	Q48656	630	1	SOR2_HUMAN	Q96pQ0	homo sapien
558	6	2.1	850	1	PSTP_HCMVA	P16724	631	1	TSP2_BOVIN	Q95116	bos taurus
559	6	2.1	854	1	ENV_FIVSD	P19030	632	1	DR3A_PSEEL	Q9xdh6	pseudomonas
560	6	2.1	855	1	ENV_FIVB8	Q04995	633	1	HELS_METUA	Q58524	methanococc
561	6	2.1	857	1	DD24_MOUSE	Q9esv0	634	1	THS_DROME	P42286	drosophila
562	6	2.1	859	1	ENV_EIAV9	P11306	635	1	NFT5_MOUSE	Q9wv30	mus musculus
563	6	2.1	859	1	ENV_EIAVC	P32541	636	1	TOP2_TRYCR	P30190	trypanosoma
564	6	2.1	859	1	ENV_EIAVW	P16082	637	1	PIB3_HUMAN	Q01970	homo sapien
565	6	2.1	859	1	ENV_EIAVY	P06751	638	1	PIB3_RAT	Q99je6	rattus norv
566	6	2.1	868	1	ACO2_SYNY3	P74582	639	1	PCGN_MOUSE	P55066	mus musculus
567	6	2.1	872	1	DNAB_SYNY3	Q55418	640	1	APU_THESA	P36905	t amylopull
568	6	2.1	872	1	GUXA_CELFI	P50401	641	1	GAX_HUMAN	Q14976	homo sapien
569	6	2.1	872	1	SYA_STRP6	Q97q48	642	1	RPOM_YEAST	P13433	saccharomyc
570	6	2.1	872	1	SYA_STRR6	Q8dpG7	643	1	PMO1_SCHPO	P13619	schizosacch
571	6	2.1	879	1	AMD2_HUMAN	Q01433	644	1	INSR_AEDAE	Q93105	aedes aegypt
572	6	2.1	881	1	HELI_HSVEB	Q01433	645	1	MRP1_YEAST	P43638	saccharomyc
573	6	2.1	882	1	SYA_SYNEB	P28934	646	1	PROS_DROME	P29617	drosophila
574	6	2.1	885	1	ASE1_YEAST	Q8dh56	647	1	RPOC_XYLFA	Q9Pa87	xyella fas
575	6	2.1	889	1	KNC3_RAT	P50275	648	1	RPOC_XYLFT	Q7a333	xyella fas
576	6	2.1	903	1	AKP1_HUMAN	Q01956	649	1	ATRN_MOUSE	Q9w60	mus musculus
577	6	2.1	904	1	YN53_YEAST	P42842	650	1	ATRN_HUMAN	Q75882	homo sapien
578	6	2.1	906	1	NPPI_MOUSE	P06802	651	1	POLG_JAEVN	P14403	j genome po
579	6	2.1	906	1	NPPI_RAT	Q924c3	652	1	TOP2_PEA	Q24308	pisum sativ
580	6	2.1	908	1	TE12_NEIMB	Q06987	653	1	SPAZ_YEAST	P23201	saccharomyc
581	6	2.1	909	1	DDRI_PANTR	Q7y743	654	1	SEL2_DROME	Q04652	drosophila
582	6	2.1	913	1	DDRI_HUMAN	Q08345	655	1	SET2_CAEEL	Q18221	caenorhabdi
583	6	2.1	915	1	SFB1_HUMAN	Q15424	656	1	NFT5_HUMAN	Q94916	homo sapien
584	6	2.1	922	1	YB1C_SCHPO	P87177	657	1	YHD5_YEAST	P38735	saccharomyc
585	6	2.1	925	1	NPPI_HUMAN	P22413	658	1	ACS2_ACEXY	Q59167	acetobacter
586	6	2.1	925	1	VPH_EPHP1	P51735	659	1	TP2B_CHICK	Q42131	gallus gall
587	6	2.1	927	1	B3AT_RAT	P23562	660	1	YF74_CAEEL	Q09221	caenorhabdi
588	6	2.1	931	1	SFB1_RAT	Q88453	661	1	VIT6_OSCBR	Q94637	oscheus br
589	6	2.1	932	1	YALA_SCHPO	P05458	662	1	RIP2_MOUSE	P97433	mus musculus
590	6	2.1	941	1	NUOG_CANBF	Q079v7	663	1	CA2B_HUMAN	P13942	homo sapien
591	6	2.1	942	1	KDGT_HUMAN	P52824	664	1	CA2B_MOUSE	Q64739	mus musculus
592	6	2.1	950	1	XRN2_HUMAN	Q9h0d6	665	1	YEW2_YEAST	P32634	saccharomyc
593	6	2.1	951	1	XRN2_MOUSE	Q9dbx1	666	1	POLG_MVEV	P05769	m genome po
594	6	2.1	961	1	VIA_EMV	P03588	667	1	TI72_HUMAN	Q14981	homo sapien
595	6	2.1	962	1	PTRA_ECO57	Q8x6m8	668	1	APU_THETU	P38536	t amylopull
596	6	2.1	962	1	PTRA_ECOLI	P05458	669	1	RRP5_HUMAN	Q14690	homo sapien
597	6	2.1	962	1	PTRA_SALTI	Q8z418	670	1	MY9B_HUMAN	Q13459	homo sapien
598	6	2.1	962	1	PTRA_SALTY	Q8zmb5	671	1	SHK1_HUMAN	Q9y566	homo sapien
599	6	2.1	972	1	KFMS_HUMAN	P07333	672	1	MOR2_SCHPO	Q9hdv6	schizosacch
600	6	2.1	976	1	VIL2_ARATH	Q81644	673	1	PXDR_HUMAN	Q9htg1	homo sapien
601	6	2.1	981	1	ENL4_HUMAN	Q9hc35	674	1	ZAN_RABIT	P57999	oryctolagus
602	6	2.1	982	1	YS96_CAEEL	Q09965	675	1	AKA6_HUMAN	Q13023	homo sapien
603	6	2.1	985	1	ENV_SFV1	P23073	676	1	ESR1_YEAST	P38111	saccharomyc
604	6	2.1	1000	1	NED4_HUMAN	P46934	677	1	FAFX_MOUSE	Q93008	h probable
605	6	2.1	1001	1	R844_YEAST	Q08162	678	1	FAFX_MOUSE	P70398	m probable
606	6	2.1	1009	1	FAK2_MOUSE	Q14289	679	1	YAO5_SCHPO	Q10105	schizosacch
607	6	2.1	1009	1	FAK2_MOUSE	Q9qvp9	680	1	THYG_BOVIN	P01267	bos taurus
608	6	2.1	1009	1	FAK2_RAT	P70600	681	1	POLG_PIFV1	Q05057	paranip yel
609	6	2.1	1018	1	ST31_MOUSE	Q99mw1	682	1	IRAL_YEAST	P18963	saccharomyc
610	6	2.1	1018	1	VGNM_BPMV	P23009	683	1	VP13_YEAST	Q07878	saccharomyc
611	6	2.1	1019	1	ST31_HUMAN	Q9bxul	684	1	CADN_HUMAN	Q9h251	homo sapien
612	6	2.1	1022	1	DPO5_YEAST	P39985	685	1	POLG_DEN2P	P12823	d genome po
613	6	2.1	1032	1	YA60_SYNY3	P72637	686	1	POLG_DEN26	P29990	d genome po
614	6	2.1	1040	1	AXOI_HUMAN	Q02246	687	1	POLG_DEN27	P29991	d genome po
615	6	2.1	1047	1	RIR1_CHLMU	Q9pl93	688	1	POLG_DEN2J	P07564	d genome po
616	6	2.1	1047	1	RIR1_CHLMU	Q84834	689	1	POLG_MNV	P06935	w genome po
617	6	2.1	1049	1	ITA5_HUMAN	P08648	690	1	POLG_JAEV1	P27395	j genome po
									POLG_JAEV5	P19110	j genome po

691	6	2.1	3432	1	POLG_JAEVJ	P32886 j genome po	764	1.7	70	1	GVPA_MICBC	P08412 microcystis
692	6	2.1	3433	1	POLG_KUNJM	P14335 k genome po	765	1.7	70	1	PRRH_THERH	P43891 thermus the
693	6	2.1	3588	1	SRF1_BACSU	P27206 bacillus su	766	1.7	70	1	RNZA_RANPI	P8dfq3 rana pipien
694	6	2.1	3803	1	TSR1_DROME	Q818u7 drosophila	767	1.7	71	1	COXA_CONMA	P05484 conus magus
695	6	2.1	4289	1	TENX_HUMAN	P22105 homo sapien	768	1.7	71	1	FTSB_BUCAL	P57496 buchnera ap
696	6	2.1	4367	1	DYHC_NEUCR	P45443 neurospora	769	1.7	71	1	GVPA_PLAAG	P9r3v0 planktothri
697	6	2.1	4655	1	LRP2_HUMAN	P98164 homo sapien	770	1.7	71	1	GVPA_PSEAN	P22453 pseudanabae
698	6	2.1	4829	1	BIR6_HUMAN	Q9nr09 homo sapien	771	1.7	71	1	YORN_TTV1	P19298 thermoprote
699	6	2.1	5147	1	PCLO_HUMAN	Q9y6v0 homo sapien	772	1.7	72	1	CCX7_CONPU	P56633 conus purpu
700	6	2.1	8797	1	CNE1_HUMAN	Q9nf91 homo sapien	773	1.7	72	1	GBG_SCHPO	P94309 schizosach
701	20	1.7	20	1	CPA7_PAPSP	P80055 papio sp. (774	1.7	72	1	HSUJ_BUCSC	O63227 buchnera ap
702	5	1.7	20	1	JHBP_BOMMO	P81627 bombyx mori	775	1.7	72	1	LHA1_RHOTE	P80588 rhodocyclus
703	5	1.7	26	1	YCX6_ODOSI	P49832 odontella s	776	1.7	72	1	RR18_ODOSI	P49505 odontella s
704	5	1.7	28	1	CHG6_MYCSM	P80673 mycobacteri	777	1.7	72	1	VPI3_BPPH6	P11130 bacterioph
705	29	1	ATPA_BRYNA	1	P26965 eryopsis ma	P26965 eryopsis ma	778	1.7	72	1	VPB_BPI86	P08711 bacterioph
706	5	1.7	29	1	H2B2_ECHES	P13282 echinus esc	779	1.7	74	1	EDDF_HUMAN	O60584 homo sapien
707	5	1.7	29	1	SODC_OLLEU	P80740 olea europa	780	1.7	74	1	SRP_SOYBN	Q07502 glycine max
708	5	1.7	30	1	END2_ONCKE	P01205 oncorhynch	781	1.7	74	1	WDNM_RAT	P14730 rattus norv
709	5	1.7	30	1	TL16_SPIOL	P81834 spinacia ol	782	1.7	74	1	YDCE_ECO57	Q8x9x8 escherichia
710	5	1.7	31	1	Y3KD_BPCHP	P19187 bacterioph	783	1.7	74	1	YV96_ANASP	Q8y9s5 anabaena sp
711	32	1	MDH_NITAL	1	P10887 nitzschia a	P10887 nitzschia a	784	1.7	75	1	SIRA_BUCAL	P57522 buchnera ap
712	36	1	PSAI_ANGLY	1	P28251 angiopteris	P28251 angiopteris	785	1.7	75	1	YDCE_SCOLI	P31992 escherichia
713	36	1	PSAI_MARPO	1	P12185 marchantia	P12185 marchantia	786	1.7	76	1	VG68_BFMD2	O64260 mycobacteri
714	36	1	PSAI_PSIU	1	Q5w110 porphyra pu	Q5w110 porphyra pu	787	1.7	76	1	YOCN_BACSU	O65381 arabidopsis
715	37	1	PTTG_PORPU	1	P51318 psilotum nu	P51318 psilotum nu	788	1.7	77	1	RUB3_ARATH	O34855 bacillus su
716	37	1	VAI_BPF2	1	P19347 bacterioph	P19347 bacterioph	789	1.7	77	1	VG9_SPV1R	O65381 arabidopsis
717	38	1	PSBY_CYAPA	1	P48272 cyanophora	P48272 cyanophora	790	1.7	78	1	Y009_BPL2	P42544 bacterioph
718	38	1	TXMI_MACGS	1	P35557 macrothela	P35557 macrothela	791	1.7	78	1	CSMA_CHLAU	P15900 spiroplasma
719	39	1	COLI_STROA	1	P01196 struthio ca	P01196 struthio ca	792	1.7	78	1	YKFF_SCOLI	Q09328 chloroflexu
720	39	1	P8BL_SYNY3	1	Q53354 synechocyst	Q53354 synechocyst	793	1.7	79	1	YZ22_METJA	P75677 escherichia
721	40	1	H2B3_ECHES	1	P13283 echinus esc	P13283 echinus esc	794	1.7	79	1	LYNX_HUMAN	Q60259 methanococ
722	44	1	PHRA_BACSU	1	Q00829 bacillus su	Q00829 bacillus su	795	1.7	80	1	NUML_HUMAN	Q9bz99 homo sapien
723	44	1	RIP3_MOMCH	1	P24817 monodica c	P24817 monodica c	796	1.7	81	1	Y791_TREPA	O00483 homo sapien
724	44	1	V85_FAPVR	1	P21403 reindeer pa	P21403 reindeer pa	797	1.7	81	1	Y070_METJA	Q83770 treponema p
725	46	1	RFOP_METJA	1	P59283 methanococ	P59283 methanococ	798	1.7	82	1	YH19_STRMU	Q60373 methanococ
726	5	1.7	49	1	Y195_BPT7	P03804 bacterioph	799	1.7	82	1	Y182_STRPN	Q848q4 streptococ
727	50	1	ATPE_BOVIN	1	P05632 bos taurus	P05632 bos taurus	800	1.7	82	1	BL52_STAAU	Q97nx1 streptococ
728	50	1	ATPE_HUMAN	1	P56381 homo sapien	P56381 homo sapien	801	1.7	83	1	DLX2_RAT	P22491 staphylococ
729	51	1	ATPE_MOUSE	1	P56382 mus musculu	P56382 mus musculu	802	1.7	83	1	DM2_MOUSE	Q94204 rattus norv
730	52	1	P468_HUMAN	1	Q0uht9 homo sapien	Q0uht9 homo sapien	803	1.7	83	1	ACP_FORPU	Q94204 rattus norv
731	52	1	V88_BPV4	1	P08352 bovine papi	P08352 bovine papi	804	1.7	83	1	Y076_NPVAC	P51280 porphyra pu
732	53	1	LECI_LATOC	1	P23306 lathyrus oc	P23306 lathyrus oc	805	1.7	84	1	Y076_NPVOP	Q06690 autographa
733	53	1	LECA_LATAR	1	P07442 lathyrus ar	P07442 lathyrus ar	806	1.7	84	1	CYB_PONNI	O10329 oxyia pseu
734	54	1	RK32_TOBAC	1	P21298 nicotiana t	P21298 nicotiana t	807	1.7	85	1	FCEG_BOVIN	P29670 pomoxis nig
735	54	1	ELA6_ADE05	1	P24934 human adeno	P24934 human adeno	808	1.7	85	1	SIX2_BUTJU	Q9bdr7 bos taurus
736	55	1	ELA6_ADE05	1	P06438 human adeno	P06438 human adeno	809	1.7	85	1	THIO_METJA	P24336 buthotus ju
737	56	1	V6K_BPHX	1	P03653 bacterioph	P03653 bacterioph	810	1.7	85	1	FCFG_CAVPO	Q57755 methanococ
738	58	1	COX1_CAPHI	1	Q36347 capra hircu	Q36347 capra hircu	811	1.7	85	1	FCFG_HUMAN	Q07249 cavia porce
739	59	1	SKCA_LEIOH	1	P13487 leirus qui	P13487 leirus qui	812	1.7	86	1	FCFG_MOUSE	P30273 homo sapien
740	59	1	SKCB_LEIOH	1	P59943 leirus qui	P59943 leirus qui	813	1.7	86	1	FCFG_PIG	P20491 mus musculu
741	59	1	SKCD_LEIOH	1	P45628 leirus qui	P45628 leirus qui	814	1.7	86	1	FCFG_PIG	Q9x826 sus scrofa
742	59	1	YAM5_CABEL	1	Q17638 caenorhabdi	Q17638 caenorhabdi	815	1.7	86	1	FCFG_RAT	P10411 rattus norv
743	60	1	Y787_RICPR	1	O05977 rickettsia	O05977 rickettsia	816	1.7	86	1	TRL_HELPY	P10143 methanococ
744	62	1	GVPA_OSCAG	1	P80996 oscillatori	P80996 oscillatori	817	1.7	86	1	YABO_BACSU	O87326 helicobacte
745	62	1	YCX5_GUITR	1	O78459 guillardia	O78459 guillardia	818	1.7	86	1	YBIC_SCOLI	P37557 bacillus su
746	63	1	Y116_RICGN	1	Q92jff rickettsia	Q92jff rickettsia	819	1.7	86	1	FLIQ_CAUCR	P41038 escherichia
747	64	1	VG24_BPMU	1	Q9ctx0 bacterioph	Q9ctx0 bacterioph	820	1.7	86	1	NDOA_PSEFL	Q07823 pseudomonas
748	65	1	Y234_BACHD	1	Q9kg78 bacillus ha	Q9kg78 bacillus ha	821	1.7	87	1	Y060_NPVAC	P14164 autographa
749	66	1	FTSB_BUCAP	1	Q8k9d5 buchnera ap	Q8k9d5 buchnera ap	822	1.7	87	1	YR54_SYNY3	P58235 synechocyst
750	66	1	GVPA_AMOPE	1	P80998 amoeboacte	P80998 amoeboacte	823	1.7	87	1	P9K_BACME	O69250 bacillus me
751	66	1	RPON_PYRAE	1	Q8zyp9 pyrobaculum	Q8zyp9 pyrobaculum	824	1.7	88	1	YTHP_BACME	P12552 bacterioph
752	67	1	Y136_VIBVU	1	Q8d3l1 vibrio vuln	Q8d3l1 vibrio vuln	825	1.7	88	1	Y109_ARCFU	O28466 archaeoglob
753	67	1	YJBS_SCOLI	1	P58036 escherichia	P58036 escherichia	826	1.7	88	1	YIM3_ARCFU	O28053 archaeoglob
754	67	1	BP74_VIBVY	1	Q7mie3 vibrio vuln	Q7mie3 vibrio vuln	827	1.7	88	1	FLIQ_ECOLI	P33134 escherichia
755	68	1	BD01_HUMAN	1	P60022 homo sapien	P60022 homo sapien	828	1.7	88	1	FLIQ_ECOLI	P54701 salmonella
756	68	1	BD01_PANTR	1	O18794 macaca mula	O18794 macaca mula	829	1.7	89	1	FLIQ_ECOLI	Q32967 mycobacteri
757	68	1	Y415_ARCFU	1	P60023 pan troglod	P60023 pan troglod	830	1.7	89	1	RS15_MYCLE	O34701 mycobacteri
758	68	1	Y415_ARCFU	1	O29832 archaeoglob	O29832 archaeoglob	831	1.7	89	1	RS15_MYCTU	P51921 pagrus majo
759	68	1	Y415_ARCFU	1	Q87mc1 rabies viru	Q87mc1 rabies viru	832	1.7	89	1	GON3_PAGMA	P51923 sparus auz
760	69	1	VC_RABVA	1	P52201 rabies viru	P52201 rabies viru	833	1.7	90	1	NULM_BRALA	O79420 branchiosto
761	70	1	GVPA_ANAFU	1	P10397 anabaena fl	P10397 anabaena fl	834	1.7	90	1		
762	70	1	GVPA_ANASP	1	Q8xfu1 anabaena sp	Q8xfu1 anabaena sp	835	1.7	90	1		
763	70	1	GVPA_FREDI	1	P07060 fremyella d	P07060 fremyella d	836	1.7	91	1		

837	5	1.7	91	1	RK23 MARPO	P06390 marchantia	910	103	1	NDOA_PSEAE	Q51493 pseudomonas
838	5	1.7	91	1	VE5A_HPV11	P04017 human papil	911	103	1	NDOA_PSEPU	P23082 pseudomonas
839	5	1.7	91	1	VE5A_HPV6A	Q84296 human papil	912	103	1	OST4_PIG	Q29381 sus scrofa
840	5	1.7	91	1	VE5A_HPV6B	P06460 human papil	913	103	1	PHS_CHICK	Q73930 g.pterin-4-
841	5	1.7	91	1	VE5A_HPV6C	P20970 human papil	914	103	1	PHS_CHICK	Q73930 g.pterin-4-
842	5	1.7	91	1	GON1_CHICK	P37042 human papil	915	103	1	SPCB_HUMAN	Q98648 homo sapien
843	5	1.7	92	1	K11B_LEIN	Q25297 leishmania	916	103	1	YF98_ARCFU	Q9mz28 pan troglod
844	5	1.7	92	1	K11C_LEIN	Q25298 leishmania	917	104	1	GRO_CAVPO	O28674 archaeoglob
845	5	1.7	92	1	KM11_LEIDO	Q36736 leishmania	918	104	1	PAP6_ECOLI	O55235 cavia porce
846	5	1.7	92	1	KM11_LEITR	Q21436 leishmania	919	104	1	YK36_YEAST	P04744 escherichia
847	5	1.7	92	1	POQD_XANCP	Q8p6m8 xanthomonas	920	105	1	INS_ONCKE	P53828 saccharomyc
848	5	1.7	92	1	SY04_RABIT	P46632 oryctolagus	921	105	1	Y679_TREPA	P04667 oncorhynchu
849	5	1.7	92	1	YK36_ARCFU	O28637 archaeoglob	922	105	1	Y679_TREPA	O83685 treponema p
850	5	1.7	93	1	PPTB_PSEAE	P42513 pseudomonas	923	105	1	Y679_TREPA	O28815 archaeoglob
851	5	1.7	93	1	VOIC_CAEEL	Q09283 caenorhabdi	924	106	1	CLPS_CHRVO	O7nrl1 chromobacte
852	5	1.7	94	1	CH10_STRAH	Q08841 staphylococ	925	106	1	COLA_HORSE	P02704 equus cabal
853	5	1.7	94	1	VE5_FCPV1	Q02258 pygmy chimp	926	106	1	CU15_WANSE	Q94984 manduca sex
854	5	1.7	94	1	Y048_BACHD	Q9kg13 bacillus ha	927	106	1	FTSB_YERFE	Q8zcp5 yersinia pe
855	5	1.7	95	1	CYB_GOMVA	P29666 gomphosus v	928	106	1	GUAU_RAT	P70668 rattus norv
856	5	1.7	95	1	GON1_SPAAU	P51919 spatus aura	929	106	1	HMGI_CRIGR	Q9qxp3 cricetus
857	5	1.7	95	1	HIS2_HALN1	Q9hmd4 halobacteri	930	106	1	KACA_RAT	P01836 rattus norv
858	5	1.7	95	1	LST1_MOUSE	O08843 mus musculu	931	106	1	KACB_RAT	P01836 rattus norv
859	5	1.7	95	1	P95_ADE02	P03286 human adeno	932	106	1	NULC_PSINU	Q8whx7 psilorum nu
860	5	1.7	95	1	YA38_SCHPO	Q09714 schizosacch	933	106	1	VNEM_CVB	P37989 chrysanthem
861	5	1.7	95	1	YC19_PORPU	P51353 porphyra pu	934	106	1	YNE3_YEAST	P33957 saccharomyc
862	5	1.7	96	1	FYR_GEOSD	P29665 geophagus s	935	107	1	COL_RABIT	P42890 oryctolagus
863	5	1.7	96	1	FER_SYNLI	P00255 synchococ	936	107	1	FTSL_HAEIN	P45058 haemophilus
864	5	1.7	96	1	HIS2_WETH	O27344 methanobact	937	107	1	QACH_STA9A	O87868 staphylococ
865	5	1.7	97	1	FER_SYNEL	P00256 synchococ	938	107	1	U258_MOUSE	O8c4x7 mus musculu
866	5	1.7	97	1	SPAC_BPT4	P39230 bacterioph	939	107	1	YFHF_HAEIN	P44672 haemophilus
867	5	1.7	97	1	VE7_COPV	Q89759 canine oral	940	107	1	YJMO_YEAST	P47020 saccharomyc
868	5	1.7	97	1	YRBB_ECOLI	P45389 escherichia	941	108	1	COLB_HORSE	P02705 equus cabal
869	5	1.7	98	1	GAS1_ATH	P46689 arabidopsis	942	108	1	HMGC_MOUSE	P52927 mus musculu
870	5	1.7	98	1	NULM_MACRO	P92667 macroopus ro	943	108	1	KVSP_MOUSE	P01649 mus musculu
871	5	1.7	98	1	NULM_ORNAN	O36457 ornithorhyn	944	108	1	SVS4_MOUSE	P18419 mus musculu
872	5	1.7	98	1	NULM_SQUAC	Q92246 squalus aca	945	108	1	YD08_METJA	O58704 methanococ
873	5	1.7	98	1	PHS_CAEEL	Q9c2h6 caenorhabdi	946	109	1	GLPM_PSEAB	P52112 pseudomonas
874	5	1.7	99	1	V55_BPT3	P20319 bacterioph	947	109	1	HMGC_HUMAN	P52926 homo sapien
875	5	1.7	99	1	APC3_MACFA	P18659 macaca fasc	948	109	1	NUOM_BOVIN	P25712 bos taurus
876	5	1.7	99	1	ESXB_MYCTU	O69739 mycobacteri	949	109	1	PRVA_FELCA	P80079 felis silve
877	5	1.7	99	1	NUOK_MYCTU	P95171 mycobacteri	950	109	1	RL3E_METKA	O8txj0 methanopyru
878	5	1.7	99	1	PSD2_BOVIN	P56701 bos taurus	951	109	1	VNST_BUNGE	P16992 bunyavirus
879	5	1.7	100	1	APC3_CANFA	P12279 canis fami	952	109	1	YK75_PSEAE	Q9hyw6 pseudomonas
880	5	1.7	100	1	BOPI_BOVIN	P83107 bos taurus	953	109	1	ZM33_MAIZE	O82106 zea mays (m
881	5	1.7	100	1	CBIN_ANASP	Q8yq90 anabaena sp	954	109	1	CYC6_FOYE	Q8wkj8 porphyra ye
882	5	1.7	100	1	NUOK_BUCBP	Q89at7 buchnera ap	955	110	1	INS_GRILO	P01313 cricetus
883	5	1.7	100	1	PTCB_BACST	O45399 bacillus st	956	110	1	VATF_XENLA	Q918h3 xenopus lae
884	5	1.7	100	1	REGN_BPP22	P04891 bacterioph	957	111	1	H2B_LEIN	P27893 leishmania
885	5	1.7	100	1	RL27_UREPA	Q9pqt2 ureaplasma	958	111	1	PRO2_BOVIN	Q09430 bos taurus
886	5	1.7	100	1	UR31_BRUME	Q8ynx6 bruceella me	959	111	1	PT09_STYPL	P28201 styela plic
887	5	1.7	100	1	UR32_BRUSU	Q8fzww bruceella su	960	111	1	Y805_CHLIE	Q8ke85 chlorobium
888	5	1.7	100	1	Y134_MYCFN	P75502 mycoplasma	961	111	1	YR23_CAEEL	Q09340 caenorhabdi
889	5	1.7	100	1	YA52_METJA	Q58452 methanococ	962	112	1	COL_CANFA	P19090 canis fami
890	5	1.7	100	1	YA74_CAVCR	O45973 caulobacter	963	112	1	COL_HUMAN	P04118 homo sapien
891	5	1.7	100	1	YJCE_BACSU	O31627 bacillus su	964	112	1	LV2K_HUMAN	P04209 homo sapien
892	5	1.7	101	1	DMT1_ALAMI	Q9puq0 alligator m	965	112	1	OL11_MOUSE	Q60890 mus musculu
893	5	1.7	101	1	RS16_URFA	Q9ppi1 ureaplasma	966	112	1	OLP3_MOUSE	Q60879 mus musculu
894	5	1.7	101	1	THST_THETS	Q9bnw4 thersonyzo	967	112	1	SVS4_RAT	P02783 rattus norv
895	5	1.7	101	1	VNST_MAGV	P16494 maguari vir	968	112	1	VE4_HPV29	P51897 human papil
896	5	1.7	101	1	YKZE_BACSU	P16605 magnayvi	969	113	1	YC4C_PSEPU	P03787 pseudomonas
897	5	1.7	101	1	YKZE_BACSU	O34356 bacillus su	970	113	1	LCCL_LEUGE	P34035 leuconostoc
898	5	1.7	101	1	CMGC_BACHD	P28670 bacillus su	971	113	1	LV1_CHICK	P04210 gallus gall
899	5	1.7	102	1	CYB_MEGAT	Q8k923 bacillus ha	972	113	1	Y544_WETH	Q26644 methanobact
900	5	1.7	102	1	HBZ_MESAU	P29627 mesocricetu	973	113	1	YAKO_YEAST	P39550 saccharomyc
901	5	1.7	102	1	HSF2_PONPY	P35301 pongo pygma	974	114	1	PARA_TRYBB	P18764 trypanosoma
902	5	1.7	102	1	PSK5_ORYSA	O81277 oryza sativ	975	114	1	FT2B_HALVA	P42198 haloarcula
903	5	1.7	102	1	YD63_BACPN	P46318 bacillus su	976	115	1	ACPM_MYCLE	Q69475 mycobacteri
904	5	1.7	102	1	YD63_BACPN	P75418 mycoplasma	977	115	1	GUAN_HUMAN	O02747 homo sapien
905	5	1.7	102	1	YU72_XANCP	Q8p6m8 xanthomonas	978	115	1	GUAN_RAT	P28902 rattus norv
906	5	1.7	102	1	YU72_XANCP	Q8p6m8 xanthomonas	979	115	1	NL41_HORVU	Q43767 hordeum vul
907	5	1.7	102	1	YU72_XANCP	P13204 bos taurus	980	115	1	RL19_COXBU	Q83685 coxiella bu
908	5	1.7	103	1	ANFB_BOVIN	Q8xny3 clostridium	981	115	1	RL20_MYCPE	Q8euk7 mycoplasma
909	5	1.7	103	1	CBIN_CLOFE		982	115	1		

983 Q9JWJ8 neisseria m
 984 P75494 mycoplasma
 985 Q9JXE2 neisseria m
 986 Q9CP59 pasteurella
 987 Q9J680 mus musculus
 988 Q9J102 strachio ca
 989 Q8CV93 leptospira
 990 Q8A174 methanococc
 991 Q46204 chlamydia p
 992 Q46182 buchnera ap
 993 P02419 escherichia
 994 P33776 tobacco rat
 995 P39504 bacterioph
 996 Q9GKY5 sus scrofa
 997 Q9XIS7 arabidopsis
 998 P07625 roseobacter
 999 Q90094 canine aden
 1000 P01774 homo sapien

ALIGNMENTS

RESULT 1
 M12A_HUMAN
 ID M12A_HUMAN STANDARD; PRT; 107 AA.
 AC P19875; Q9UPB8;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Macrophage inflammatory protein-2-alpha precursor (MIP2-alpha) (CXCL2)
 DE (Growth regulated protein beta) (Gro-beta).
 GN CXCL2 OR GRO2 OR SCYB2 OR GROB OR MIP2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Histocytic lymphoma;
 RX MEDLINE=90354792; PubMed=2201751;
 RA Tekamp-Olson F., Gallegos C., Bauer D., McClain J., Sherry B.,
 RA Fabre M., van Deventer S., Cerami A.;
 RT "Cloning and characterization of cDNAs for murine macrophage
 RT inflammatory protein 2 and its human homologues";
 RL J. Exp. Med. 172:911-919 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90377259; PubMed=2078213;
 RA Iida N., Grotendorst G.R.;
 RT "Cloning and sequencing of a new gro transcript from activated human
 RT monocytes: expression in leukocytes and wound tissue";
 RL Mol. Cell. Biol. 10:5596-5599 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91017578; PubMed=2217207;
 RA Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
 RA Smith T., Martin G., Ralph P., Sager R.;
 RT "Identification of three related human GRO genes encoding cytokine
 RT functions";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736 (1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP SEQUENCE OF 35-107 FROM N.A.
 RA Jang J.S., Kim B.B.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP STRUCTURE BY NMR OF 39-107.
 RX MEDLINE=20069929; PubMed=10600366;
 RA Cilan Y.O., Johanson K.O., McDevitt P.;
 RT "Nuclear magnetic resonance solution structure of truncated human
 RT GRObeta [5-73] and its structural comparison with CXCL chemokine
 RT family members GROalpha and IL-8";
 RL J. Mol. Biol. 294:1065-1072 (1999).
 CC -!- FUNCTION: Produced by activated monocytes and neutrophils and
 CC expressed at sites of inflammation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
 CC family.
 CC -----
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 CC -----
 CC EMBL; X53799; CAA37808.1; -;
 CC EMBL; M36820; AAA63183.1; -;
 CC EMBL; M57731; AAA63182.1; -;
 CC EMBL; BC015753; AAH15753.1; -;
 CC EMBL; AF043340; AAC03540.1; -;
 CC PIR; JH0281; JH0281.
 CC PDB; 1QNK; 04-FEB-00.
 CC Genew; HGNC:4603; CXCL2.
 CC MIM; 139110; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0008009; F:chemokine activity; TAS.
 CC GO; GO:0006935; P:chemotaxis; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC InterPro; IPR001811; Chemokine IL8.
 CC InterPro; IPR001089; CXC_chemokine_sm1.
 CC Pfam; PF00048; IL8; 1.
 CC SMART; SM00199; SCY; 1.
 CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
 FT 2-ALPHA.
 FT DISULFID 43 69
 FT DISULFID 45 85
 FT STRAND 49 49
 FT TURN 54 56
 FT STRAND 57 63
 FT STRAND 73 78
 FT TURN 79 80
 FT STRAND 83 86
 FT TURN 88 89
 FT TURN 93 95
 FT TURN 98 102
 SEQUENCE 107 AA; 11389 MW; 740F277E928571BA CRC64;

Query Match 2.8%; Score 8; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

167 LLLLVAAAS 174
22 LLLLVAAAS 29

RESULT 2
M12B HUMAN STANDARD; PRT; 107 AA.
ID MI2B HUMAN STANDARD; PRT; 107 AA.
AC P19876;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Macrophage inflammatory protein-2-beta precursor (MIP2-beta) (CXCL3)
DE (Growth regulated protein gamma) (GRO-gamma).
GN CXCL3 OR GRO3 OR SCYB3 OR GROG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Histocytic lymphoma;
RX MEDLINE=90354792; PubMed=2201751;
RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA Fabre M., van Deventer S., Cerami A.;
RA "Cloning and characterization of cDNAs for murine macrophage
inflammatory protein 2 and its human homologues.";
RL J. Exp. Med. 172:911-919(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91017578; PubMed=2217207;
RA Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA Smith T., Martin G., Ralph P., Sager R.;
RA "Identification of three related human GRO genes encoding cytokine
functions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22398257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a role in inflammation and exert its effects on
endothelial cells in an autocrine fashion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxcl)
family.
CC
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EMBL; X53800; AAA37809.1; -;
EMBL; M36821; AAA63184.1; -;
EMBL; BC016308; AAH16308.1; -;
PIR; JH0282; B38290.
HSSP; P19875; LONK.
Genew; HGNC:4604; CXCL3.
MIM; 139111; -;
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0008009; F:chemokine activity; TAS.
InterPro; IPR001811; Chemokine IL8.
InterPro; IPR001089; CXC_chemkine_smll.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 34
FT CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
2-BETA.
FT DISULFID 43 69 BY SIMILARITY.
FT DISULFID 45 85 BY SIMILARITY.
FT CONFLICT 27 28 AA -> G (IN REF. 2).
FT SEQUENCE 107 AA; 11342 MW; 97A69946B7F1F070 CRC64;
Query Match 2.8%; Score 8; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

167 LLLLVAAAS 174
22 LLLLVAAAS 29

RESULT 3
SY04 MOUSE STANDARD; PRT; 92 AA.
ID SY04 MOUSE STANDARD; PRT; 92 AA.
AC P14097;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).
GN CCL4 OR SCYA4 OR MIP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89067830; PubMed=3058856;
RA Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,
RA Wolpe S.D., Masiazz F., Coit D., Cerami A.;
RA "Resolution of the two components of macrophage inflammatory protein
1, and cloning and characterization of one of those components,
macrophage inflammatory protein 1 beta.";
RL J. Exp. Med. 168:2251-2259(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RA "A family of small inducible proteins secreted by leukocytes are
members of a new superfamily that includes leukocyte and fibroblast-
derived inflammatory agents, growth factors, and indicators of various
activation processes.";
RL J. Immunol. 142:679-687(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/2J; TISSUE=Liver;

RA Dauberries P., Lepretre F., Bailleul B., Grove M., Pragnell I.,
 RA Plumb M.A., Submitted (Oct-1991) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Oct-1991) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=10.S/J, and SJL/J; TISSUE=Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teucher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.,
 RA "Sequence polymorphisms in the chemokines Sclav (TCA-3), Scya2
 RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/relapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M23503; AAA40148.1; -.
 DR EMBL; M35590; AAA39708.1; -.
 DR EMBL; X62502; CAA4364.1; -.
 DR EMBL; AF128218; AAF22559.1; -.
 DR EMBL; AF128219; AAF22560.1; -.
 DR PIR; C30552; C30552.
 DR HSP; P13236; IHUM.
 DR MGD; MGI:98261; Ccl4.
 DR InterPro; IPR000827; CC chemokine sm1.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.
 FT DISULFID 34 58 BY SIMILARITY.
 FT DISULFID 35 74 BY SIMILARITY.
 SQ SEQUENCE 92 AA; 10168 MW; 8853FD58FDE61BAC CRC64;
 Query Match 2.4%; Score 7; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 LLLVAA 173
 Db 10 LLLVAA 16
 RESULT 4
 SY04 RAT
 ID SY04 RAT STANDARD; PRT; 92 AA.
 AC P50230;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 10-OCT-1996 (Rel. 34, Last sequence update)
 DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
 DE protein 1-beta) (MIP-1-beta).
 GN CCL4 OR SCYA4 OR MIP1B.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Long Evans; TISSUE=Lung;

RA Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;
 RL Submitted (Feb-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U06434; AAA36497.1; -.
 DR HSP; P13236; IHUM.
 DR InterPro; IPR000827; CC chemokine sm1.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.
 FT DISULFID 34 58 BY SIMILARITY.
 FT DISULFID 35 74 BY SIMILARITY.
 SQ SEQUENCE 92 AA; 10234 MW; 60B451EEBC7103D CRC64;
 Query Match 2.4%; Score 7; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 LLLVAA 173
 Db 10 LLLVAA 16
 RESULT 5
 GROG_BOVIN
 ID GROG_BOVIN STANDARD; PRT; 98 AA.
 AC O46675;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Growth regulated protein homolog gamma precursor (GRO-gamma).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152812; PubMed=10028286;
 RA Modi W.S., Yoshimura T.,
 RT "Isolation of novel GRO genes and a phylogenetic analysis of the CXCR
 RT chemokine subfamily in mammals.";
 RL Mol. Biol. Evol. 16:180-193(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CXCR)
 CC family.
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 CC EMBL; U95811; AAB93927.1; -.
 DR HSP; P19875; 1QNK.
 DR InterPro; IPR001811; Chemokine_IL8.

```
DR InterPro; IPR001089; CXK_chmkine_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR000437; SMALLCYTKCXC.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine; Growth factor; Inflammatory response; Signal.
KW SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 98 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 98 AA; 10393 MW; 942CD6897C21EDE9 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 18 LLLLVAA 24

RESULT 6
GRO_SHEEP
ID GRO_SHEEP STANDARD; PRT; 103 AA.
AC 046678;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Growth regulated protein precursor (CXCL1).
GN CXCL1 OR SCVB1 OR GRO.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152612; PubMed=10028286;
RA Medi W.S., Yoshimura T.;
RT "Isolation of novel GRO genes and a phylogenetic analysis of the CXK
chekokine subfamily in mammals."
RL Mol. Biol. Evol. 16:180-193(1999).
CC -!- FUNCTION: Has chemotactic activity for neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxk)
family.
-----
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EMBL; U95814; AAB93930.1; -
HSP; P19875; IONK.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR001089; CXK_chmkine_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCXC.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine; Growth factor; Inflammatory response; Signal.
KW SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 104 GROWTH REGULATED PROTEIN HOMOLOG.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10900 MW; 10B9D07B65C77F67 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 19 LLLLVAA 25

RESULT 8
GRO_BOVIN
ID GRO_BOVIN STANDARD; PRT; 104 AA.
AC 046677;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Growth regulated protein homolog beta precursor (GRO-beta).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
```

MEDLINE=95105175; PubMed=7806518;
Kim K.S., Clark-Lewis I., Sykes B.D.;
"Solution structure of GRO/melanoma growth stimulatory activity
determined by 1H NMR spectroscopy.";
J. Biol. Chem. 269:32909-32915(1994).
-!- FUNCTION: Has chemotactic activity for neutrophils. May play a
role in inflammation and exerts its effects on endothelial cells
in an autocrine fashion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cx) family.

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EMBL; J03561; AAA35933.1; -;
EMBL; X12510; CAA31027.1; -;
EMBL; X54489; CAA39361.1; -;
EMBL; BC011976; AAL11976.1; -;
PIR; S13669; A28414.
PDB; 1MSG; 30-SEP-94.
PDB; 1MSG; 31-MAR-95.
PDB; 1MSH; 31-MAR-95.
PDB; 1ROD; 10-JUN-96.
Gene; HGNC:4602; CXCL1.
MIM; 155730; -;
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0008009; F:chemokine activity; TAS.
GO; GO:0008047; F:enzyme activator activity; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0007242; P:intracellular signaling cascade; TAS.
GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
GO; GO:0007401; P:pan-neural process; TAS.
InterPro; IPR001811; Chemokine_IL8.
InterPro; IPR001089; CXCL1_chemokine_sm1.
Pfam; PF00048; IL8; 1.
PRINTS; PR00437; SMALLCYTCKC.
SMART; SM0199; SCY; 1.
PROSITE; PS00471; SMALL CYTOKINES CX; 1.
Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
SIGNAL 1 34 GROWTH REGULATED PROTEIN.
FT CHAIN 35 107
FT DISULFID 43 69
FT DISULFID 45 85
FT TURN 44 45
FT STRAND 49 49
FT TURN 54 56
FT STRAND 57 63
FT STRAND 73 78
FT TURN 79 80
FT STRAND 83 86
FT TURN 88 89
FT HELIX 91 103
FT TURN 104 104
FT SEQUENCE 107 AA; 11301 MW; 17049A6B4D765CA2 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 LLLLVAA 173
DB 22 LLLLVAA 28

RESULT 10
YB76_AQUAE STANDARD; PRT; 111 AA.
ID YB76_AQUAE
AC O67237;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1176.
GN AQ_1176.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
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EMBL; AB000727; AAC07206.1; -;
PIR; B70401; B70401.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 111 AA; 12958 MW; C38490CB2FF25B19 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 DOVEVEY 236
DB 38 DOVEVEY 44

RESULT 11
LY96_CRIGR STANDARD; PRT; 160 AA.
ID LY96_CRIGR
AC P587E5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 96 precursor (MD-2 protein).
GN LY96 OR MD2.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT TYR-95.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=21329172; PubMed=11435474;
RA Schromm A.B., Lien E., Henneke P., Chow J.C., Yoshimura A., Heine H.,
RA Latz E., Monks B.G., Schwartz D.A., Miyake K., Golenbock D.T.;
RT "Molecular genetic analysis of an endotoxin nonresponder mutant cell
line. A point mutation in a conserved region of MD-2 abolishes
endotoxin-induced signaling.";
J. Exp. Med. 194:79-88(2001).
RL -!- FUNCTION: Cooperates with TLR4 in the innate immune response to
bacterial lipopolysaccharide (LPS), and with TLR2 in the response

to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TLR4-dependent activation of NF- κ B. Cells expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS (BY similarity).

-!- SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (BY similarity).

-!- SUBCELLULAR LOCATION: Extracellular.

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EMBL: AF325501; AAK57984.1; -
InterPro: IPR003172; E1_DerF2_DerF2.
Pfam: PF02221; E1_DerF2_DerF2; 1.
SMART: SM00737; ML; 1.
Immune response; Inflammatory response; Signal; Glycoprotein; Polymorphism.

FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 160 LYMPHOCYTE ANTIGEN 96.
FT DISULFID 95 105 BY SIMILARITY.
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 95 95 C -> Y (IN ENDOTOXIN NONRESPONDER).
SQ SEQUENCE 160 AA; 18357 MW; 0B533B1AA5B46DD6 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 LIPLIFT 164
DB 10 LIPLIFT 16

RESULT 12
YMS7 PSEAE
ID YMS7 PSEAE STANDARD; PRT; 171 AA.
AC Q9H767,
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical ANK-repeat protein PA3287.
GN PA3287
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkman F.S.H., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltser S., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -!- SIMILARITY: Contains 3 ANK repeats.

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EMBL: AEO04751; AAG06675.1; -
PIR: H83233; H83233.
InterPro: IPR002110; ANK.
Pfam: PF00023; ank; 4.
DR SMART: SM00248; ANK; 3.
DR PROSITE: PS0088; ANK_REPEAT; 3.
DR PROSITE: PS0297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat; Complete proteome.
FT REPEAT 48 77
FT REPEAT 81 110 ANK 2.
FT REPEAT 114 143 ANK 3.
SQ SEQUENCE 171 AA; 18194 MW; 16C0C8A47120E03C CRC64;

Query Match 2.4%; Score 7; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 VAASLLA 177
DB 130 VAASLLA 136

RESULT 13
FARP CAEEL
ID FARP CAEEL STANDARD; PRT; 175 AA.
AC FA1855;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE FMRamide-like neuropeptides precursor.
GN FLP-1 OR F23B2.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=Bristol N2;
RX MEDLINE=92300457; PubMed=1607945;
RA Rosoff M.L., Buerklin T.R., Li C.;
RT "Alternatively spliced transcripts of the flp-1 gene encode distinct FMRamide-like peptides in Caenorhabditis elegans.";
RL J. Neurosci. 12:2356-2361 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE=93248060; PubMed=8483810;
RA Rosoff M.L., Doble K.E., Price D.A., Li C.;
RT "The flp-1 propeptide is processed into multiple, highly similar FMRamide-like peptides in Caenorhabditis elegans.";
RL Peptides 14:331-338 (1993).
CC -!- FUNCTION: May function as a hormone.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing, Named isoforms-2;
CC Name=Long;
CC IsoId=P41855-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P41855-2; Sequence=VSP_001563;
CC Notes=Expressed at about a twofold higher level than isoform Long;
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)

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CC family.
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CC -----
DR EMBL; S38096; AAC22368.1; -
DR EMBL; U00670; AAC46464.1; -
DR EMBL; Z82266; CAB05179.1; -
DR PIR; B44827; B44827.
DR PIR; T21297; T21297.
DR WormPep; F23B2.5; CE09585.
DR InterPro; IPR002544; FARP.
DR Pfam; PF01581; FARP; 8.
KW Neuropeptide; Amidation; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 21
FT PROPEP 22 67
FT PEPTIDE 71 76 PNFVRY-AMIDE.
FT PROPEP 79 86
FT PEPTIDE 89 98 AGSDPNFLRF-AMIDE.
FT PEPTIDE 101 108 SGNPNFLRF-AMIDE.
FT PEPTIDE 111 120 ASGDPNFLRF-AMIDE.
FT PEPTIDE 123 130 SDPNFLRF-AMIDE (PF1).
FT PEPTIDE 133 142 AAADPNFLRF-AMIDE.
FT PROPEP 146 154 SADPNFLRF-AMIDE (PF2).
FT PEPTIDE 157 165
FT PEPTIDE 168 173 PNFNLF-AMIDE.
FT MOD_RES 76 76 AMIDATION (G-77 PROVIDE AMIDE GROUP).
FT MOD_RES 98 98 AMIDATION (G-99 PROVIDE AMIDE GROUP).
FT MOD_RES 108 108 AMIDATION (G-109 PROVIDE AMIDE GROUP).
FT MOD_RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP).
FT MOD_RES 130 130 AMIDATION (G-131 PROVIDE AMIDE GROUP).
FT MOD_RES 142 142 AMIDATION (G-143 PROVIDE AMIDE GROUP).
FT MOD_RES 154 154 AMIDATION (G-155 PROVIDE AMIDE GROUP).
FT MOD_RES 173 173 AMIDATION (G-174 PROVIDE AMIDE GROUP).
FT VARSPPLIC 81 91 Missing (in isoform Short).
FT SEQUENCE 175 AA; 19705 MW; 8888DF266B59E7F CRC64;
Query Match 2.4%; Score 7; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 LLLLVAA 173
DB 9 LLLLVAA 15
RESULT 14
RRF_NEIMA
ID RRF_NEIMA STANDARD; PRT; 185 AA.
AC Q9UR52;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome recycling factor (Ribosome releasing factor) (RRF).
GN RRF OR NMA0080 OR NME0187.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

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RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone K., Clark E.B.,
RA Cotton M.D., Utterback T.R., Knouri H., Qin H., Vamathevan J.,
RA Gill J., Scariato V., Maignani V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Responsible for the release of ribosomes from messenger
CC RNA at the termination of protein biosynthesis. May increase the
CC efficiency of translation by recycling ribosomes from one round of
CC translation to another (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the RRF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL162752; CAB83396.1; -
DR EMBL; AF002375; AAF40644.1; -
DR PIR; D81229; D81229.
DR HSSP; Q9X1B9; 1DD5.
DR TIGR; NME0187; -
DR HAMAP; MF_00040; -; 1.
DR InterPro; IPR002661; RRF.
DR Pfam; PF01765; RRF; 1.
DR ProDom; PD004103; RRF; 1.
DR TIGRFAMs; TIGR00496; frr; 1.
KW Protein biosynthesis; Complete proteome.
SQ SEQUENCE 185 AA; 20731 MW; 668D1C347B846603 CRC64;
Query Match 2.4%; Score 7; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 230 DQVEVEY 236
DB 38 DQVEVEY 44
RESULT 15
HA19_MOUSE
ID HA19_MOUSE STANDARD; PRT; 200 AA.
AC P14431;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE H-2 class I histocompatibility antigen, Q9 alpha chain precursor
DE (Fragment).
GN H2-Q9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10;
RX MEDLINE=86135949; PubMed=3004940;
RA Devlin J.J., Weiss E.H., Paulson M., Flavell R.A.;
RT "Duplicated gene pairs and alleles of class I genes in the Qa2 region
of the murine major histocompatibility complex: a comparison.";
RL EMBO J. 4:3203-3207(1985).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X03443; CAA27172.1; ALT_INIT.
DR HSP: P16391; 1ED3.
DR MGD: MGI:95938; H2-Q9.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001039; MHC I.
DR Pfam: PF00129; MHC I; 1.
DR PRINTS: PR01638; MHCCLASS1.
DR ProDom: PD000050; MHC I; 1.
DR PROSITE: PS00290; IG_MHC; PARTIAL.
KW MHC I; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 >200
FT -----
FT H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT Q9 ALPHA CHAIN.
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 22 111
FT DOMAIN 112 >200
FT DISULFID 122 185
FT CARBOHYD 107 107
FT NON_TER 200 200
FT SEQUENCE 200 AA; 23025 MW; 4C2B7E2D059EA82E CRC64;
FT -----
Query Match 2.4%; Score 7; DB 1; Length 200;
Best Local Similarity 100.0%; Pred.No.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 167 LLLLVAA 173
DB 6 LLLLVAA 12
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Search completed: September 16, 2004, 12:52:35
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:48:26 / Search time 116 Seconds
(without alignments)
788.796 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290
Sequence: 1 MPLLTLVLLFWLSGYSIAT.....SXLPGRGPBPTEYSTISRP 290

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	166	57.2	290	4	Q7Z6A6
2	149	51.4	244	4	Q8NAF5
3	137	47.2	290	4	Q8TDQ1
4	134	46.2	194	4	Q8N6D0
5	120	41.4	293	4	Q7Z715
6	71	24.5	165	4	Q7Z714
7	10	3.4	201	4	Q8IX40
8	10	3.4	238	4	Q8N6D1
9	9	3.1	472	16	Q7WEK0
10	9	3.1	472	16	Q7W381
11	9	3.1	545	10	Q8SLI2
12	9	3.1	1102	16	Q88CW3
13	9	3.1	3956	2	Q7WTF2
14	8	2.8	149	13	O57313
15	8	2.8	186	4	Q8UMT0
16	8	2.6	221	11	Q6BRU3

221	11	Q8VCH2	Q8vch2 mus musculu
264	16	Q88NT2	Q88nt2 pseudomonas
283	11	Q8K4V9	Q8k4v9 mus musculu
298	4	Q9HD97	Q9hd97 homo sapien
299	4	Q9UGN4	Q9ugn4 homo sapien
299	4	Q9UBK4	Q9ubk4 homo sapien
301	4	Q9S100	Q9s100 homo sapien
374	10	Q8SBD0	Q8sbd0 oryza sativ
395	16	Q89ZL3	Q89zl3 bacteroides
475	16	Q8YM67	Q8ym67 arabidopsi
484	16	Q9KYG5	Q9kyg5 streptomyce
600	17	Q980K5	Q980k5 sulfolobus
674	10	Q94E29	Q94e29 oryza sativ
695	5	Q86LL4	Q86ll4 giardia lam
708	5	P91954	P91954 lucilia cup
813	16	Q8XZJ7	Q8xzj7 ralestonia s
24	7	Q861J2	Q861j2 rattus norv
36	16	Q8F1V7	Q8f1v7 leptospira
64	16	Q89DM0	Q89dm0 bradyrhizob
76	10	Q84PU7	Q84pu7 oryza sativ
80	2	Q9RHX1	Q9rxh1 corynebacte
91	16	Q825L2	Q825l2 streptomyce
99	17	Q97Z64	Q97z64 sulfolobus
109	11	Q60639	Q60639 mus musculu
109	11	Q62653	Q62653 rattus norv
120	16	Q9IYW2	Q9iYW2 neisseria m
120	16	Q9A4P5	Q9a4p5 caulobacter
125	2	O5J123	O5j123 mycobacteri
142	5	Q81I22	Q81i22 caenorhabdi
145	8	Q94QD8	Q94qd8 crotalus tr
145	16	Q9KQ01	Q9kq01 vibrio chol
151	10	Q9FFX3	Q9ffy3 arabidopsis
158	16	Q7VX71	Q7vx71 bordetella
162	16	Q7WLI4	Q7wli4 bordetella
162	16	Q7W837	Q7w837 bordetella
164	5	Q23805	Q23805 caenorhabdi
164	10	Q8LI24	Q8li24 oryza sativ
166	2	Q93D76	Q93d76 bacillus th
167	2	Q7X0E5	Q7x0e5 staphylococ
167	2	Q7X0E4	Q7x0e4 staphylococ
167	10	Q8LDK5	Q8ldk5 arabidopsis
167	10	Q9SACS	Q9sacs arabidopsis
172	15	Q86689	Q86689 feline immu
172	15	Q9PXX9	Q9pxk9 feline immu
174	5	Q23806	Q23806 caenorhabdi
184	7	Q9CZ20	Q9cz20 mus musculu
187	17	Q9YER3	Q9yer3 aeropyrum p
190	2	Q93D74	Q93d74 bacillus th
190	5	Q9GYC2	Q9gyc2 leishmania
192	16	Q8ZNI5	Q8zni5 salmoneilla
194	16	Q9A9U0	Q9a9u0 caulobacter
198	10	Q9ARPI	Q9arp1 oryza sativ
198	10	Q7XXK6	Q7xxk6 oryza sativ
202	10	Q8GW95	Q8gw95 arabidopsis
208	5	Q8SV33	Q8sv33 encephalito
210	2	Q938B2	Q938b2 anaplasma c
210	16	Q55649	Q55649 synecocyst
215	16	Q98H67	Q98h67 rhizobium l
218	5	Q9TZF3	Q9tzf3 caenorhabdi
230	2	Q8X71	Q8x71 aeromonas h
233	16	Q8RR77	Q8rr77 staphylococ
233	16	Q83CV2	Q83cv2 coxiella bu
244	16	Q88YA5	Q88ya5 lactobacill
253	10	Q84RW0	Q84rw0 oryza sativ
253	16	Q8EHF5	Q8ehf5 shewanella
256	16	Q89CQ5	Q89cq5 bradyrhizob
257	17	Q9UZG4	Q9uzg4 pyrococcus
258	2	Q9ZNF2	Q9znf2 staphylococ
258	2	Q9EZM3	Q9ezm3 staphylococ
260	5	Q870Z3	Q870z3 triatoma in
265	16	Q98DT6	Q98dt6 rhizobium l
270	11	Q8R159	Q8r159 mus musculu

90	7	2.4	273	2	Q68480	Q68480 achromobact	163	7	2.4	452	11	Q8BN13	Q8bn13 mus musculus
91	7	2.4	283	16	Q6FSW7	Q8f5w7 leptospira	164	7	2.4	462	16	Q8AT3	Q8at3 pseudomonas
92	7	2.4	283	16	Q8EK9	Q8ek9 shewanella	165	7	2.4	464	16	Q8ET1	Q8et1 shewanella
93	7	2.4	284	16	Q8RV15	Q8rv15 delinococcus	166	7	2.4	465	10	Q8LJ43	Q8lj43 oryza sativ
94	7	2.4	284	16	Q8YCN9	Q8ycn9 brucella me	167	7	2.4	465	10	Q8LJ43	Q8lj43 oryza sativ
95	7	2.4	287	16	Q8K877	Q8k877 bacillus ha	168	7	2.4	468	16	Q8WH5	Q8wh5 bordetella
96	7	2.4	289	3	Q101090	Q101090 kluyveromyc	169	7	2.4	476	4	Q8YH17	Q8yh17 homo sapien
97	7	2.4	290	16	Q8AL80	Q8al80 brucella su	170	7	2.4	477	4	Q8YH17	Q8yh17 homo sapien
98	7	2.4	292	16	Q8Y176	Q8yl76 ralatonia s	171	7	2.4	478	16	Q8L1RW3	Q8l1rw3 bacillus an
99	7	2.4	293	16	Q8O896	Q8o896 salmonella	172	7	2.4	480	10	Q8S212	Q8s212 oryza sativ
100	7	2.4	295	13	Q8J132	Q8j132 oncornynchu	173	7	2.4	500	16	Q8KD12	Q8kd12 chlorobium
101	7	2.4	299	16	Q8I092	Q8i092 pseudomonas	174	7	2.4	508	12	Q8S579	Q8s579 bovine herp
102	7	2.4	301	16	Q8ZNH5	Q8znh5 streptomyce	175	7	2.4	508	12	Q8S5821	Q8s5821 bovine herp
103	7	2.4	304	4	Q8NEP4	Q8nep4 homo sapien	176	7	2.4	519	16	Q8Z708	Q8z708 chlamydia p
104	7	2.4	308	16	Q89FP4	Q89fp4 bradyrhizob	177	7	2.4	520	10	Q6S815	Q6s815 helianthus
105	7	2.4	309	16	Q89VY4	Q89vy4 staphylococ	178	7	2.4	521	6	Q46651	Q46651 cryctolagus
106	7	2.4	311	17	Q8Y8U7	Q8y8u7 aeropyrum p	179	7	2.4	521	6	Q46634	Q46634 canis famil
107	7	2.4	312	2	Q8VQS9	Q8vqs9 staphylococ	180	7	2.4	522	16	Q8G2H8	Q8g2h8 brucella su
108	7	2.4	312	16	Q8ERN3	Q8ern3 bradyrhizob	181	7	2.4	524	10	Q8G7K2	Q8g7k2 oryza sativ
109	7	2.4	314	11	Q7TNS3	Q7tns3 mus musculus	182	7	2.4	533	16	Q8YFE2	Q8yfe2 brucella me
110	7	2.4	318	11	Q8CFN3	Q8cfn3 mus musculus	183	7	2.4	533	17	Q8V0J2	Q8v0j2 pyrococcus
111	7	2.4	318	11	Q7TNS6	Q7tns6 mus musculus	184	7	2.4	537	2	Q8EZ98	Q8ez98 zymomonas m
112	7	2.4	319	16	Q8CFI8	Q8cfi8 lactococcus	185	7	2.4	538	16	Q8KRN1	Q8krn1 vibrio chol
113	7	2.4	320	16	Q8ZL57	Q8zlb7 streptomyce	186	7	2.4	539	5	Q8T4G6	Q8t4g6 drosophila
114	7	2.4	324	2	Q8KIK7	Q8kik7 rhizobium e	187	7	2.4	539	10	Q8LN93	Q8ln93 arabidopsis
115	7	2.4	326	7	P79567	P79567 mus musculus	188	7	2.4	539	16	Q8RD59	Q8rd59 streptomyce
116	7	2.4	326	7	P79568	P79568 mus musculus	189	7	2.4	539	16	Q87P06	Q87p06 vibrio para
117	7	2.4	327	17	Q9V2H9	Q9v2h9 pyrococcus	190	7	2.4	543	2	Q8L868	Q8l868 desulfovibr
118	7	2.4	328	7	Q11199	Q11199 mus musculus	191	7	2.4	543	16	Q8P8R5	Q8p8r5 xanthomonas
119	7	2.4	329	12	Q8JPS7	Q8jps7 corriparta	192	7	2.4	547	5	Q9VD53	Q9vd53 drosophila
120	7	2.4	331	2	Q87492	Q87492 staphylococ	193	7	2.4	549	10	Q8LN87	Q8ln87 arabidopsis
121	7	2.4	331	16	Q99XA0	Q99xa0 staphylococ	194	7	2.4	550	4	Q8N4X7	Q8n4x7 homo sapien
122	7	2.4	331	16	Q8RCZ2	Q8rcz2 thermoanaer	195	7	2.4	554	15	Q87107	Q87107 chimpanzee
123	7	2.4	331	16	Q8NVS8	Q8nvs8 staphylococ	196	7	2.4	557	9	Q8SD93	Q8sd93 pseudomonas
124	7	2.4	331	16	Q8NRZ3	Q8nrz3 corynebacte	197	7	2.4	558	5	Q8IH53	Q8ih53 drosophila
125	7	2.4	336	2	Q7X2Z2	Q7x2z2 uncultured	198	7	2.4	560	13	Q7T0S1	Q7t0s1 xenopus lae
126	7	2.4	338	16	Q8R9Q8	Q8r9q8 rhizobium m	199	7	2.4	561	11	Q8BPC8	Q8bpc8 mus musculu
127	7	2.4	341	13	Q90WF6	Q90wf6 gallus gall	200	7	2.4	561	16	Q82BG1	Q82bg1 streptomyce
128	7	2.4	341	13	Q90644	Q90644 gallus gall	201	7	2.4	562	3	Q9UVB9	Q9uvb9 pichia cife
129	7	2.4	345	2	Q8L2N0	Q8l2n0 bacillus th	202	7	2.4	563	11	Q8B172	Q8bi72 mus musculu
130	7	2.4	349	5	Q95Y11	Q95y11 caenorhabdi	203	7	2.4	570	4	Q8N821	Q8n821 homo sapien
131	7	2.4	357	16	Q7Y47	Q7y47 mycobacteri	204	7	2.4	572	10	Q8VYV8	Q8vym8 arabidopsis
132	7	2.4	358	17	Q970G1	Q970g1 sulfobolus	205	7	2.4	579	4	Q8TBM5	Q8tbm5 homo sapien
133	7	2.4	363	11	Q8B151	Q8bi51 mus musculu	206	7	2.4	580	4	Q9NXV6	Q9nxv6 homo sapien
134	7	2.4	363	17	Q97BF1	Q97bf1 thermoplasma	207	7	2.4	588	16	Q8PMA4	Q8pma4 xanthomonas
135	7	2.4	366	10	Q93Y71	Q93y71 oryza sativ	208	7	2.4	592	16	Q83A98	Q83a98 coxiella bu
136	7	2.4	372	2	Q86182	Q86182 streptomyce	209	7	2.4	593	4	Q7Z3F9	Q7z3f9 homo sapien
137	7	2.4	373	7	Q861Q1	Q861q1 rattus norv	210	7	2.4	595	12	Q83896	Q83896 ovine adeno
138	7	2.4	378	16	Q8DJ51	Q8djs1 synchococ	211	7	2.4	596	17	Q8TRM8	Q8trm8 methanosarc
139	7	2.4	380	16	Q8ZHL7	Q8zhl7 versinia pe	212	7	2.4	598	3	Q871F6	Q871f6 neurospora
140	7	2.4	387	3	Q86ZX7	Q86zx7 conidiobol	213	7	2.4	598	16	Q8PHX4	Q8phx4 xanthomonas
141	7	2.4	391	17	Q979S3	Q979s3 thermoplasma	214	7	2.4	598	17	Q29907	Q29907 archaeoglob
142	7	2.4	394	16	Q7VIF4	Q7vif4 prochloroco	215	7	2.4	599	16	Q8KAF2	Q8kaf2 bacillus ha
143	7	2.4	400	5	Q9BJM2	Q9bjm2 litomosoid	216	7	2.4	600	16	Q8P6M0	Q8p6m0 xanthomonas
144	7	2.4	401	5	Q968A6	Q968a6 plasmodium	217	7	2.4	600	16	Q89QG3	Q89qg3 bradyrhizob
145	7	2.4	407	16	Q8XU94	Q8xu94 ralatonia s	218	7	2.4	617	11	Q54766	Q54766 rattus norv
146	7	2.4	410	16	Q8RJ38	Q8rj38 streptomyce	219	7	2.4	627	16	Q7UQW4	Q7uqw4 rhodospirall
147	7	2.4	412	2	Q7WVY3	Q7wv3 alcaligenes	220	7	2.4	631	4	Q8NYH0	Q8nyh0 homo sapien
148	7	2.4	414	16	Q8XU02	Q8xu02 ralatonia s	221	7	2.4	634	4	Q8TAE4	Q8tae4 homo sapien
149	7	2.4	415	10	Q9AS33	Q9as33 oryza sativ	222	7	2.4	634	11	Q8BTU3	Q8btu3 mus musculu
150	7	2.4	416	16	Q67172	Q67172 aquifex aeo	223	7	2.4	635	4	Q989Y5	Q989y5 homo sapien
151	7	2.4	417	16	Q7TYQ0	Q7tyq0 mycobacteri	224	7	2.4	642	16	Q2S396	Q2s396 helicobacte
152	7	2.4	419	16	Q986W4	Q986w4 rhizobium l	225	7	2.4	642	16	Q8ZLF3	Q8zlf3 helicobacte
153	7	2.4	421	16	Q98LZ7	Q98lz7 rhizobium l	226	7	2.4	652	5	Q9W0G4	Q9w0g4 drosophila
154	7	2.4	422	2	Q9F826	Q9f826 micromonosop	227	7	2.4	657	2	Q93D79	Q93d79 bacillus th
155	7	2.4	422	16	Q9K7U0	Q9k7u0 bacillus ha	228	7	2.4	658	16	Q8P3D2	Q8p3d2 xanthomonas
156	7	2.4	430	16	P71757	P71757 mycobacteri	229	7	2.4	661	5	Q9M185	Q9m185 drosophila
157	7	2.4	441	4	Q86UN2	Q86un2 homo sapien	230	7	2.4	662	5	Q8IR58	Q8irs8 drosophila
158	7	2.4	444	10	Q8H3C8	Q8h3c8 oryza sativ	231	7	2.4	665	2	Q845T2	Q845t2 vibrio vuln
159	7	2.4	445	5	Q9W478	Q9w478 drosophila	232	7	2.4	665	16	Q8D5B0	Q8d5b0 vibrio vuln
160	7	2.4	449	2	Q93EJ5	Q93ej5 bacillus li	233	7	2.4	675	8	Q9TAJ6	Q9taj6 cafeteria r
161	7	2.4	452	11	Q9DD22	Q9dd22 mus musculu	234	7	2.4	687	5	Q8SXR7	Q8sxr7 drosophila
162	7	2.4	452	11	Q99LJ1	Q99lj1 mus musculu	235	7	2.4	687	10	Q948Y7	Q948y7 volvox cart

236	7	2.4	694	11	Q8CFT6	Q8ctf6 mus musculus	309	7	2.4	4283	11	Q9ERV0	Q9erv0 rattus norv
237	7	2.4	697	5	Q8IH79	Q8ih79 drosophila	310	7	2.4	4368	5	Q61851	Q61851 caenorhabdi
238	7	2.4	704	5	Q95XQ7	Q95xq7 caenorhabdi	311	7	2.4	4717	3	Q94248	Q94248 scizosacch
239	7	2.4	707	11	Q8QW65	Q8Qw65 mus musculus	312	6	2.1	10	12	Q39958	Q39958 hepatitis g
240	7	2.4	722	16	Q8DHZ8	Q8dhz8 synthecococ	313	6	2.1	23	9	Q8W5S4	Q8W5S4 bacterioph
241	7	2.4	731	16	Q87BR9	Q87br9 xylella fas	314	6	2.1	27	2	Q44952	Q44952 borrelia bu
242	7	2.4	751	12	Q39294	Q39294 equine herp	315	6	2.1	28	8	Q9G663	Q9G663 typanocryp
243	7	2.4	756	16	Q8CQU1	Q8cm1 pasteurella	316	6	2.1	29	2	Q9R4D5	Q9R4D5 eubacterium
244	7	2.4	763	16	Q8EAB7	Q8eab7 shewanella	317	6	2.1	30	16	Q8EAT6	Q8eat6 shewanella
245	7	2.4	769	4	Q8NB10	Q8nb10 homo sapien	318	6	2.1	32	12	Q9FWS8	Q9fws8 sindbis vir
246	7	2.4	786	10	Q9FWJ2	Q9fwj2 arabidopsis	319	6	2.1	33	10	Q94IS3	Q94is3 pinus radia
247	7	2.4	788	16	Q827F5	Q827f5 streptomyce	320	6	2.1	34	2	Q9R529	Q9r529 escherichia
248	7	2.4	789	2	Q45793	Q45793 bacillus th	321	6	2.1	36	8	Q85FL2	Q85fl2 adiantum ca
249	7	2.4	789	2	Q69270	Q69270 bacillus th	322	6	2.1	39	2	Q9RIJ8	Q9rij8 streptococ
250	7	2.4	789	2	Q45792	Q45792 bacillus th	323	6	2.1	40	10	Q94IS0	Q94is0 pinus radia
251	7	2.4	789	2	Q8R8Z5	Q8rs25 bacillus th	324	6	2.1	50	10	Q41532	Q41532 triticum ae
252	7	2.4	789	2	Q338Z1	Q938z1 bacillus th	325	6	2.1	50	12	Q9Z0S3	Q9z0s3 hepatitis g
253	7	2.4	797	4	Q96B75	Q96b75 homo sapien	326	6	2.1	50	12	Q9Z046	Q9z046 hepatitis g
254	7	2.4	801	16	Q8CPU8	Q8cpus staphylococ	327	6	2.1	51	15	Q9QGE7	Q9qge7 human immun
255	7	2.4	802	5	Q95QC4	Q95qc4 caenorhabdi	328	6	2.1	52	4	Q8NHT5	Q8nht5 homo sapien
256	7	2.4	812	4	Q8N0W6	Q8n0w6 homo sapien	329	6	2.1	53	16	Q8ZRC7	Q8zrc7 salmonella
257	7	2.4	829	10	Q8L7V3	Q8l7v3 arabidopsis	330	6	2.1	55	16	Q87FG1	Q87fg1 vibrio para
258	7	2.4	837	5	Q8I2A5	Q8c2a5 dictyosteli	331	6	2.1	58	9	Q03908	Q03908 bacterioph
259	7	2.4	849	10	Q7XSS2	Q7xss2 oryza sativ	332	6	2.1	59	5	Q61591	Q61591 osteritagia
260	7	2.4	878	16	Q99ZF1	Q99zf1 streptococ	333	6	2.1	59	10	Q9SBC7	Q9sbc7 leavenworth
261	7	2.4	878	16	Q8P0U3	Q8p0u3 streptococ	334	6	2.1	59	10	Q81686	Q81686 leavenworth
262	7	2.4	878	16	Q8K7B4	Q8k7b4 streptococ	335	6	2.1	59	10	Q81681	Q81681 leavenworth
263	7	2.4	890	4	Q8N277	Q8n277 homo sapien	336	6	2.1	59	10	Q82815	Q82815 leavenworth
264	7	2.4	900	16	Q92Z67	Q92z67 rhizobium m	337	6	2.1	59	10	Q81678	Q81678 leavenworth
265	7	2.4	909	4	Q8N3F3	Q8n3f3 homo sapien	338	6	2.1	59	10	Q81683	Q81683 leavenworth
266	7	2.4	925	2	Q9F4J0	Q9f4j0 porphyronon	339	6	2.1	59	10	Q81684	Q81684 leavenworth
267	7	2.4	929	4	Q8N973	Q8n973 homo sapien	340	6	2.1	59	10	Q81687	Q81687 leavenworth
268	7	2.4	969	4	Q86V43	Q86v43 homo sapien	341	6	2.1	59	10	Q81682	Q81682 leavenworth
269	7	2.4	985	2	Q9ZNI6	Q9zni6 pseudomonas	342	6	2.1	59	10	Q81685	Q81685 leavenworth
270	7	2.4	988	10	Q9FWV2	Q9fwv2 oryza sativ	343	6	2.1	59	10	Q8S573	Q8s573 catharanthu
271	7	2.4	988	10	Q7XD45	Q7xd45 oryza sativ	344	6	2.1	61	10	Q8C5B7	Q8c5b7 arabidopsis
272	7	2.4	1009	16	Q8U8W1	Q8u8w1 agrobacteri	345	6	2.1	62	4	Q8WX05	Q8wx05 homo sapien
273	7	2.4	1010	16	Q9X8M9	Q9x8m9 streptomyce	346	6	2.1	62	5	Q7YVA8	Q7yva8 trypanosoma
274	7	2.4	1013	4	Q9NT81	Q9nt81 homo sapien	347	6	2.1	62	16	Q98NP7	Q98np7 rhizobium l
275	7	2.4	1015	4	Q8N3X1	Q8n3x1 homo sapien	348	6	2.1	64	9	Q9XJ52	Q9xj52 bacterioph
276	7	2.4	1023	5	Q9KYD4	Q9kyd4 dictyosteli	349	6	2.1	65	2	Q9FCZ0	Q9fcz0 erwinia ste
277	7	2.4	1050	4	Q9Y2L7	Q9y2l7 homo sapien	350	6	2.1	65	2	Q85378	Q85378 lactococcus
278	7	2.4	1058	11	Q9QYS4	Q9qys4 mus musculus	351	6	2.1	65	16	Q8YGM2	Q8ygm2 brucella me
279	7	2.4	1058	11	Q9QZX2	Q9qzx2 mus musculus	352	6	2.1	65	16	Q8G193	Q8g193 brucella su
280	7	2.4	1058	11	Q8CDH7	Q8cdh7 mus musculus	353	6	2.1	66	11	Q9QWE3	Q9qwe3 mus sp. alp
281	7	2.4	1060	5	Q86AN6	Q86an6 dictyosteli	354	6	2.1	66	17	Q9YCD4	Q9ycd4 aeropyrum p
282	7	2.4	1063	5	Q9U699	Q9u699 drosophila	355	6	2.1	68	5	Q8VNR7	Q8vnr7 caenorhabdi
283	7	2.4	1063	5	Q9TVM2	Q9tvm2 drosophila	356	6	2.1	68	16	Q8AAD1	Q8aad1 bacteroides
284	7	2.4	1067	16	Q9RZQ3	Q9rzq3 deinococcus	357	6	2.1	70	5	Q9SPA9	Q9spa9 conus texti
285	7	2.4	1089	16	Q9HTT4	Q9htt4 pseudomonas	358	6	2.1	71	5	Q9BPA7	Q9bpa7 conus penna
286	7	2.4	1103	5	Q27721	Q27721 plasmodium	359	6	2.1	72	5	Q9BFB1	Q9bfb1 conus texti
287	7	2.4	1151	5	Q96993	Q96993 heterodera	360	6	2.1	72	10	Q8S9N3	Q8s9n3 oryza sativ
288	7	2.4	1184	16	Q05435	Q05435 mycobacteri	361	6	2.1	73	2	Q9X5W9	Q9x5w9 pantoea cit
289	7	2.4	1184	16	Q7TVJ1	Q7tvd1 mycobacteri	362	6	2.1	73	5	Q9BPA4	Q9bpa4 conus texti
290	7	2.4	1185	11	Q8CHA4	Q8cha4 mus musculus	363	6	2.1	73	5	Q9BPA2	Q9bpa2 conus texti
291	7	2.4	1208	5	Q8I5I3	Q8i5t3 plasmodium	364	6	2.1	73	5	Q9BPA5	Q9bpa5 conus texti
292	7	2.4	1228	5	Q27724	Q27724 plasmodium	365	6	2.1	73	16	Q8YIA1	Q8yia1 ralstonia s
293	7	2.4	1242	3	Q60103	Q60103 schizosacch	366	6	2.1	74	5	Q9BPD0	Q9bpd0 conus ventr
294	7	2.4	1264	5	Q9U445	Q9u445 plasmodium	367	6	2.1	74	5	Q9BPC9	Q9bpc9 conus ventr
295	7	2.4	1332	16	Q8PFO6	Q8pfg6 xanthomonas	368	6	2.1	75	5	Q9BPA9	Q9bpa9 conus tessu
296	7	2.4	1399	5	Q7YVJ2	Q7yvjj2 trypanosoma	369	6	2.1	76	2	Q9JA63	Q9ja63 gamma-prote
297	7	2.4	1430	13	Q7ZZ58	Q7zz58 brachydanio	370	6	2.1	76	2	Q9BPA8	Q9bpa8 conus texti
298	7	2.4	1498	5	Q7YZS4	Q7yzs4 physarum po	371	6	2.1	76	5	Q9BPA6	Q9bpa6 conus ventr
299	7	2.4	1540	10	Q9SGX4	Q9sgx4 arabidopsis	372	6	2.1	76	5	Q9BPA7	Q9bpa7 conus texti
300	7	2.4	1639	13	Q8Q4W6	Q8q4w6 fugu rubrip	373	6	2.1	76	10	Q9ZTA6	Q9zta6 hordeum vul
301	7	2.4	2110	3	Q8XIE9	Q8xie9 emericeila	374	6	2.1	76	10	Q91FF0	Q91ff0 arabidopsis
302	7	2.4	2370	16	Q82RE3	Q82re3 streptomyce	375	6	2.1	76	16	Q8E8Q1	Q8e8q1 shewanella
303	7	2.4	2479	11	Q63002	Q63002 rattus norv	376	6	2.1	77	5	Q9BPA7	Q9bpa7 conus ventr
304	7	2.4	2491	4	Q96PT5	Q96pt5 homo sapien	377	6	2.1	77	5	Q9BPA6	Q9bpa6 conus penna
305	7	2.4	2491	4	Q7Z7G9	Q7z7g9 homo sapien	378	6	2.1	77	5	Q9BPA6	Q9bpa6 conus penna
306	7	2.4	3898	12	Q8Q8A0	Q8q8a0 bovine vira	379	6	2.1	77	5	Q9BPC2	Q9bpc2 conus ventr
307	7	2.4	4032	2	Q7WTF3	Q7wtf3 streptomyce	380	6	2.1	77	5	Q9BPC8	Q9bpc8 conus ventr
308	7	2.4	4197	12	Q807Z8	Q807z8 bovine vira	381	6	2.1	77	16	Q88N08	Q88n08 pseudomonas

382	6	2.1	78	5	QBFB0	QBpb0 conus texti	455	6	2.1	108	16	Q9R6B5	Q9r6b5 agrobacteri
383	6	2.1	78	10	Q945D8	Q945d8 castanea sa	456	6	2.1	109	2	Q44379	Q44379 agrobacteri
384	6	2.1	78	17	Q972V0	Q972v0 sulfolobus	457	6	2.1	109	3	Q02613	Q02613 saccharomyc
385	6	2.1	79	5	QBpPC5	QBpPC5 conus ventr	458	6	2.1	109	16	Q8A671	Q8a671 bacteroides
386	6	2.1	79	10	Q39807	Q39807 glycine max	459	6	2.1	109	17	Q9VEB4	Q9yeb4 aeropyrum p
387	6	2.1	79	12	Q8JMS3	Q8jms3 mamestra co	460	6	2.1	110	2	Q8KVM2	Q8kvw2 ruigeria sp
388	6	2.1	79	16	Q9EXU7	Q9exu7 rhizobium m	461	6	2.1	110	9	Q9r1B0	Q9r1b0 bacterioph
389	6	2.1	79	16	Q8Z107	Q8z107 salmonella	462	6	2.1	110	11	Q8CQ41	Q8cq41 mus musculu
390	6	2.1	80	4	Q9NS95	Q9ns95 homo sapien	463	6	2.1	110	16	Q8r419	Q8r4y9 listeria mo
391	6	2.1	80	5	QBpPA8	QBpPA8 conus penna	464	6	2.1	111	2	Q9A126	Q9a126 escherichia
392	6	2.1	80	16	Q8YY47	Q8yy47 anabaena sp	465	6	2.1	111	5	Q9V9E8	Q9v9e8 drsophila
393	6	2.1	80	16	Q8E404	Q8e404 streptococ	466	6	2.1	112	11	Q8CBW0	Q8cbw0 mus musculu
394	6	2.1	81	2	Q8S908	Q8s908 shingomona	467	6	2.1	112	3	Q08498	Q08498 saccharomyc
395	6	2.1	81	5	QBpHA0	QBpHA0 conus texti	468	6	2.1	113	10	Q81675	Q81675 leavenworth
396	6	2.1	81	12	Q914G2	Q914g2 sulfolobus	469	6	2.1	113	10	Q81674	Q81674 leavenworth
397	6	2.1	82	10	Q8L698	Q8l698 triticum ae	470	6	2.1	113	10	Q81673	Q81673 leavenworth
398	6	2.1	83	2	Q9XB44	Q9xb44 escherichia	471	6	2.1	113	16	Q83167	Q83167 tropheryma
399	6	2.1	84	2	Q34283	Q34283 yersinia pe	472	6	2.1	113	16	Q83F27	Q83f27 tropheryma
400	6	2.1	84	12	Q55747	Q55747 chilo iride	473	6	2.1	113	16	Q7V5G4	Q7v5g4 prochloroco
401	6	2.1	85	2	Q9461	Q9461 mycoplasma	474	6	2.1	113	16	Q7U9D0	Q7u9d0 synechococc
402	6	2.1	85	16	Q8FPN9	Q8fpn9 corynebacte	475	6	2.1	114	16	Q9RK45	Q9rk45 streptomyce
403	6	2.1	85	17	Q8ZXF0	Q8zxf0 pyrobaculum	476	6	2.1	114	16	Q8A8U9	Q8a8u9 bacteroides
404	6	2.1	86	2	Q49641	Q49641 mycobacteri	477	6	2.1	114	16	Q87RF3	Q87rf3 vibrio para
405	6	2.1	87	16	Q8XW88	Q8xw88 ralatonia s	478	6	2.1	115	16	Q839F9	Q839f9 enterococu
406	6	2.1	87	16	Q8P6G5	Q8p6g5 xanthomonas	479	6	2.1	115	16	Q81KC0	Q81kc0 bacillus an
407	6	2.1	88	16	Q8V522	Q8v522 listeria mo	480	6	2.1	116	8	Q85D52	Q85d52 esox lucius
408	6	2.1	89	9	Q852Y9	Q852y9 mycobacteri	481	6	2.1	116	17	Q9VFM4	Q9vfm4 aeropyrum p
409	6	2.1	90	4	Q96FS8	Q96fs8 homo sapien	482	6	2.1	117	5	Q81G02	Q81g02 caenorhabdi
410	6	2.1	90	16	Q8RSN8	Q8rsn8 deinococcus	483	6	2.1	117	16	Q87CU7	Q87cu7 xylella fas
411	6	2.1	91	13	Q8UWJ2	Q8uwj2 gallus gall	484	6	2.1	117	16	Q87CA6	Q87ca6 xylella fas
412	6	2.1	91	16	Q9PCW8	Q9pcw8 xylella fas	485	6	2.1	118	5	Q16344	Q16344 caenorhabdi
413	6	2.1	92	2	Q45127	Q45127 bacillus ps	486	6	2.1	118	5	Q95PE0	Q95pe0 anhyomma a
414	6	2.1	93	16	Q82LD8	Q82ld8 streptomyc	487	6	2.1	118	15	Q40450	Q40450 human immun
415	6	2.1	94	11	Q8CF72	Q8cf72 mus musculu	488	6	2.1	118	16	Q92G60	Q92g60 rickettsia
416	6	2.1	95	16	Q88X00	Q88x00 lactobacill	489	6	2.1	119	11	Q8K477	Q8k477 rattus norv
417	6	2.1	95	16	Q833U5	Q833u5 enterococu	490	6	2.1	119	16	Q7WH73	Q7wh73 bordetella
418	6	2.1	96	16	Q8X374	Q8x374 escherichia	491	6	2.1	119	16	Q7W917	Q7w917 bordetella
419	6	2.1	97	1	Q9C4X1	Q9c4x1 sulfolobus	492	6	2.1	119	16	Q7VWP4	Q7vwp4 bordetella
420	6	2.1	97	6	Q8MIT7	Q8mit7 macaca mula	493	6	2.1	120	6	Q29206	Q29206 sus scrofa
421	6	2.1	97	6	Q8HXZ5	Q8hxz5 macaca mula	494	6	2.1	120	16	Q821J8	Q821j8 salmonella
422	6	2.1	97	16	Q98A16	Q98a16 rhizobium l	495	6	2.1	120	16	Q7UPT2	Q7upt2 rhodopirell
423	6	2.1	98	8	Q9G6Q5	Q9g6q5 diplophos t	496	6	2.1	121	16	Q9KMM1	Q9kmm1 vibrio chol
424	6	2.1	98	16	Q8YUJ3	Q8yuJ3 anabaena sp	497	6	2.1	122	2	Q49269	Q49269 mycoplasma
425	6	2.1	98	16	Q81RH9	Q81rh9 bacillus an	498	6	2.1	123	11	Q8BR67	Q8br67 mus musculu
426	6	2.1	99	9	Q8SCN5	Q8scn5 pseudomonas	499	6	2.1	123	11	Q8C614	Q8c614 mus musculu
427	6	2.1	100	6	Q95MD5	Q95md5 bos taurus	500	6	2.1	124	16	Q87PE2	Q87pe2 vibrio para
428	6	2.1	100	12	Q3VU50	Q3vus0 turkey aden	501	6	2.1	124	16	Q7UVZ5	Q7uvz5 rhodopirell
429	6	2.1	100	16	Q8P6H9	Q8p6h9 xanthomonas	502	6	2.1	124	17	Q972R6	Q972r6 sulfolobus
430	6	2.1	100	16	Q89VG0	Q89vg0 bradyrhizob	503	6	2.1	125	4	Q9NV40	Q9nv40 homo sapien
431	6	2.1	100	16	Q9RPM3	Q9rpm3 salmonella	504	6	2.1	125	5	Q8WRC7	Q8wrc7 manduca sex
432	6	2.1	100	17	Q96Z72	Q96z72 sulfolobus	505	6	2.1	125	12	Q7TA18	Q7ta18 sars corona
433	6	2.1	101	4	Q86YV5	Q86yv5 homo sapien	506	6	2.1	125	16	Q88BP3	Q88bp3 pseudomonas
434	6	2.1	101	11	Q91Z64	Q91z64 sigmodon hi	507	6	2.1	125	16	Q87QU9	Q87qu9 vibrio para
435	6	2.1	101	16	Q8HV19	Q8hv19 pseudomonas	508	6	2.1	125	16	Q7U412	Q7u412 synechococc
436	6	2.1	101	16	Q8ER14	Q8er14 oceanobacil	509	6	2.1	127	4	Q9HBR3	Q9hbr3 homo sapien
437	6	2.1	102	4	Q9P1K8	Q9p1k8 homo sapien	510	6	2.1	127	6	Q04209	Q04209 ovis sp. ov
438	6	2.1	102	11	Q8C3P2	Q8c3p2 mus musculu	511	6	2.1	127	11	Q9CVR1	Q9cvr1 mus musculu
439	6	2.1	103	5	Q19451	Q19451 caenorhabdi	512	6	2.1	127	16	Q92VJ9	Q92vj9 rhizobium m
440	6	2.1	103	10	Q8S7P5	Q8s7p5 oryza sativ	513	6	2.1	127	16	Q8D4D5	Q8d4d5 vibrio vuln
441	6	2.1	104	2	Q7WWY1	Q7wwy1 alcaligenes	514	6	2.1	128	3	Q8X1Y8	Q8x1y8 kluyveromyc
442	6	2.1	104	4	Q9H050	Q9h050 homo sapien	515	6	2.1	128	4	Q96SH5	Q96sh5 homo sapien
443	6	2.1	104	10	Q9XJ72	Q9xj72 cucumis sat	516	6	2.1	128	11	Q80ZT4	Q80zt4 mus musculu
444	6	2.1	104	17	Q9JG82	Q9jg82 aeropyrum p	517	6	2.1	128	16	Q802T4	Q802t4 mus musculu
445	6	2.1	105	6	Q9GLC5	Q9glc5 bos taurus	518	6	2.1	128	16	Q88P63	Q88p63 pseudomonas
446	6	2.1	106	3	Q9HE66	Q9he66 neurospora	519	6	2.1	129	11	Q8VDR4	Q8vdr4 mus musculu
447	6	2.1	106	10	Q93359	Q93359 nicotiana t	520	6	2.1	129	16	Q912K6	Q912k6 pseudomonas
448	6	2.1	106	12	Q82001	Q82001 human papil	521	6	2.1	130	6	Q8EUF5	Q8euf5 mycoplasma
449	6	2.1	107	2	Q938S0	Q938s0 pseudomonas	522	6	2.1	130	10	Q9FK01	Q9fk01 arabidopsis
450	6	2.1	107	2	Q51606	Q51606 citrobacter	523	6	2.1	131	16	Q8PMB6	Q8pmb6 xanthomonas
451	6	2.1	107	6	Q8HXZ4	Q8hxz4 macaca mula	524	6	2.1	131	16	Q9PAL4	Q9pal4 xanthomonas
452	6	2.1	107	6	Q8HXZ3	Q8hxz3 macaca mula	525	6	2.1	132	4	Q75768	Q75768 homo sapien
453	6	2.1	108	2	Q49237	Q49237 mycoplasma	526	6	2.1	132	16	Q888F7	Q888f7 pseudomonas
454	6	2.1	108	10	Q8W0J8	Q8w0j8 oryza sativ	527	6	2.1	133	2	Q93F13	Q93f13 shigella fl

528	6	2.1	133	10	Q94X8	Q94X8 brassica na	601	151	11	Q9DA47	Q9da47 mus musculu
529	6	2.1	133	10	Q9S9F5	Q9s9f5 citrullus l	602	151	16	Q9ZQ16	Q9zq16 rhizobium m
530	6	2.1	133	16	Q99U85	Q99u85 staphylococ	603	151	16	Q8NTM9	Q8ntm9 corynebacte
531	6	2.1	134	17	Q9Y9B7	Q9y9b7 aeropyrum p	604	151	16	Q827S6	Q827s6 streptomyce
532	6	2.1	135	11	Q8BM36	Q8bm36 mus musculu	605	152	16	Q8E9N9	Q8e9n9 shewanella
533	6	2.1	135	16	Q82RQ3	Q82rq3 streptomyce	606	153	4	Q8NFX0	Q8nfx0 homo sapien
534	6	2.1	135	5	Q8MOY5	Q8moy5 drosophila	607	153	4	Q8P004	Q8p004 homo sapien
535	6	2.1	136	6	Q9GL21	Q9gl21 macaca fasc	608	153	4	Q7Z4E5	Q7z4e5 homo sapien
536	6	2.1	137	2	Q9S394	Q9s394 mycoplasma	609	153	7	Q9XR15	Q9xr15 equus caball
537	6	2.1	137	11	Q9CVL6	Q9cvl6 mus musculu	610	153	11	Q9CQZ0	Q9cqz0 mus musculu
538	6	2.1	137	11	Q9CSJ7	Q9csj7 mus musculu	611	153	13	Q42210	Q42210 necturus ma
539	6	2.1	137	16	Q81H29	Q81h29 bacillus ce	612	153	13	Q82RR6	Q82rr6 streptomyce
540	6	2.1	137	17	Q26321	Q26321 methanobact	613	154	2	Q8KNL0	Q8knl0 salmonella
541	6	2.1	138	5	Q95Y93	Q95y93 caenorhabdi	614	154	8	Q8MOD3	Q8mod3 amoebidium
542	6	2.1	138	16	Q8YR56	Q8yr56 anabaena sp	615	154	11	Q8BNQ0	Q8bnq0 mus musculu
543	6	2.1	139	2	Q8VIX9	Q8vix9 leptospira	616	154	11	Q8OYI9	Q8oyi9 mus musculu
544	6	2.1	139	2	Q9AB55	Q9ab55 leptospira	617	154	16	Q9K0G1	Q9k0g1 neisseria m
545	6	2.1	139	4	Q9BSX3	Q9bsx3 homo sapien	618	154	5	P83387	P83387 caenorhabdi
546	6	2.1	139	4	Q86SX2	Q86sx2 homo sapien	619	156	5	Q9PL49	Q9pl49 chlamydia m
547	6	2.1	139	16	Q9RSF2	Q9rsf2 deinococcus	620	156	16	Q9JTL8	Q9jtl8 neisseria m
548	6	2.1	139	16	Q88J71	Q88j71 rhizobium l	621	156	16	Q8DEE8	Q8dee8 vibrio vuln
549	6	2.1	139	16	Q8KD00	Q8kd00 chlorobium	622	156	16	Q93IN7	Q93in7 salmonella
550	6	2.1	139	16	Q9S4G1	Q9s4g1 leptospira	623	156	16	Q82DQ2	Q82dq2 streptomyce
551	6	2.1	139	16	Q7V985	Q7v985 pyrochloroco	624	157	10	Q22480	Q22480 oryza sativ
552	6	2.1	140	2	Q93MGO	Q93mgo thioabacillu	625	158	4	Q9UN54	Q9un54 homo sapien
553	6	2.1	140	3	Q9Y8D2	Q9y8d2 cochllobolu	626	158	5	Q02430	Q02430 dirofilaria
554	6	2.1	140	16	Q98G74	Q98g74 rhizobium l	627	158	5	Q85SC1	Q8esc1 penaeus jap
555	6	2.1	140	16	Q68750	Q68750 yersinia pe	628	158	5	Q8PAY5	Q8pay5 xanthomonas
556	6	2.1	140	16	Q934X7	Q934x7 salmonella	629	160	2	Q9AG92	Q9ag92 bdellovibri
557	6	2.1	140	17	Q9YD09	Q9yd09 aeropyrum p	630	160	2	Q9EY90	Q9ey90 corynebacte
558	6	2.1	140	17	Q9HI77	Q9hi77 thermoplasm	631	160	2	Q9EUL3	Q9eul3 corynebacte
559	6	2.1	141	10	Q40849	Q40849 picea glauc	632	160	16	Q8ZK30	Q8zk30 salmonella
560	6	2.1	142	2	Q52137	Q52137 escherichia	633	160	16	Q8Z117	Q8z117 salmonella
561	6	2.1	142	2	Q9AJ18	Q9aj18 escherichia	634	161	10	Q9AY91	Q9ay91 oryza sativ
562	6	2.1	142	16	Q85634	Q85634 escherichia	635	162	10	Q9ZVG1	Q9zvg1 arabidopsis
563	6	2.1	142	17	Q58906	Q58906 pyrococcus	636	162	16	Q8EYI0	Q8eyi0 leptospira
564	6	2.1	143	4	Q9H7F1	Q9h7f1 homo sapien	637	162	16	Q7WM36	Q7wm36 vibrio para
565	6	2.1	143	16	Q7UP01	Q7up01 rhodopirell	638	163	10	Q7Y0A1	Q7y0a1 oryza sativ
566	6	2.1	143	17	Q93721	Q93721 pyrobaculum	639	163	12	P87622	P87622 cowpox viru
567	6	2.1	144	2	Q49381	Q49381 mycoplasma	640	163	16	Q913W3	Q913w3 pseudomonas
568	6	2.1	144	10	Q93XN9	Q93xn9 solanum tub	641	163	16	Q8HVA1	Q8hva1 pseudomonas
569	6	2.1	144	10	Q84WQ8	Q84wq8 oryza sativ	642	163	16	Q8X9Z5	Q8x9z5 escherichia
570	6	2.1	144	10	Q84IB8	Q84ib8 oryza sativ	643	163	16	Q9ZPM3	Q9zpm3 rhizobium m
571	6	2.1	144	13	Q9W731	Q9w731 acipenser r	644	163	16	Q8DSP5	Q8dsp5 streptococc
572	6	2.1	144	16	Q8KE32	Q8ke32 chlorobium	645	163	16	Q7UDS8	Q7uds8 shigella fl
573	6	2.1	144	16	Q8DPC2	Q8ddc2 vibrio vuln	646	163	16	Q7U9N8	Q7u9n8 synechococc
574	6	2.1	145	5	Q96353	Q96353 drosophila	647	164	8	Q7VAL9	Q7val9 chara vulga
575	6	2.1	145	13	Q8JJC4	Q8jjc4 anguilla ja	648	164	16	Q9K9P1	Q9kp91 vibrio chol
576	6	2.1	145	16	Q8C311	Q8c311 staphylococ	649	164	16	Q9KDM2	Q9kdm2 bacillus ha
577	6	2.1	145	16	Q89QF9	Q89qf9 bradyrhizob	650	164	16	Q8ZIG2	Q8zig2 yersinia pe
578	6	2.1	146	3	Q8TFL6	Q8tfl6 candida gla	651	164	16	Q87SR9	Q87sr9 vibrio para
579	6	2.1	146	10	Q7XAD0	Q7xad0 lycopersico	652	164	16	Q8Z9H6	Q8z9h6 salmonella
580	6	2.1	146	11	Q9D3B3	Q9d3b3 mus musculu	653	165	4	Q9UFX5	Q9ufx5 homo sapien
581	6	2.1	147	1	Q977R2	Q977r2 uncultured	654	165	11	Q8C5Z3	Q8c5z3 mus musculu
582	6	2.1	147	2	Q57241	Q57241 streptomyce	655	165	16	Q8ZKI0	Q8zki0 salmonella
583	6	2.1	147	10	Q8S0H7	Q8s0h7 oryza sativ	656	165	16	Q8Z1T7	Q8z1t7 salmonella
584	6	2.1	148	5	Q9VJ35	Q9vj35 drosophila	657	165	16	Q82DZ7	Q82dz7 streptomyce
585	6	2.1	148	5	Q86E71	Q86e71 schistosoma	658	166	10	Q9XIX6	Q9xix6 oryza sativ
586	6	2.1	148	10	Q9AT13	Q9at13 solanum tub	659	166	10	Q7XRE9	Q7xre9 oryza sativ
587	6	2.1	148	16	Q8PQ15	Q8pq15 xanthomonas	660	166	16	Q25397	Q25397 helicobacte
588	6	2.1	149	16	Q8EYU8	Q8eyu8 leptospira	661	166	16	Q8NQK4	Q8nck4 corynebacte
589	6	2.1	150	2	Q9ZGK5	Q9zgk5 leptospira	662	166	16	Q8JTE9	Q8j9e9 pseudomonas
590	6	2.1	150	4	Q95973	Q95973 homo sapien	663	167	5	Q9QE0	Q9qe0 cryptospori
591	6	2.1	150	10	Q8H8W3	Q8h8w3 oryza sativ	664	167	8	Q48256	Q48256 dennyus cyp
592	6	2.1	150	10	Q8H3B6	Q8h3b6 oryza sativ	665	167	12	Q91KX0	Q91kx0 japanese en
593	6	2.1	150	11	Q8C219	Q8c219 mus musculu	666	167	16	Q9YX42	Q9yx42 arabanaa sp
594	6	2.1	151	2	P71490	P71490 methyloicr	667	168	8	Q48255	Q48255 dennyus vau
595	6	2.1	151	5	Q9GP20	Q9gp20 globodera r	668	168	10	Q39475	Q39475 closterium
596	6	2.1	151	10	Q8M3G6	Q8m3g6 oryza sativ	669	168	10	Q8H0X5	Q8h0x5 arabidopsis
597	6	2.1	151	10	Q7XBU7	Q7xbu7 oryza sativ	670	168	10	Q8W480	Q8w480 arabidopsis
598	6	2.1	151	11	Q62488	Q62488 mus musculu	671	168	12	Q11859	Q11859 avian infec
599	6	2.1	151	11	Q925P0	Q925p0 rattus norv	672	168	12	Q11858	Q11858 avian infec
600	6	2.1	151	11	Q8C4X3	Q8c4x3 mus musculu	673	168	16	Q99VW4	Q99vw4 staphylococ

674	6	2.1	168	16	QBNN4	Q8nn14 corynebacte	747	6	2.1	179	5	Q8GH60	Q86h60 dictyosteli
675	6	2.1	168	17	Q26967	Q26967 methanobact	748	6	2.1	179	5	Q7UW08	Q7UW08 rhodospirall
676	6	2.1	169	5	Q8MKM4	Q8mkM4 drosophila	749	6	2.1	180	5	Q7YX37	Q7YX37 caenorhabdi
677	6	2.1	169	10	Q8S6P9	Q8s6P9 oryza sativ	750	6	2.1	181	13	Q8AY40	Q8ay40 oncornynchu
678	6	2.1	170	7	Q88210	Q88210 gadus morhu	751	6	2.1	181	16	Q8E8P9	Q8e8P9 shewanella
679	6	2.1	170	10	Q84MW9	Q84mw9 oryza sativ	752	6	2.1	181	16	Q8D1B3	Q8d1B3 versinia pe
680	6	2.1	170	11	Q9CPU1	Q9cpU1 mus musculu	753	6	2.1	181	16	Q87FW6	Q87fw6 vibrio para
681	6	2.1	170	11	Q9CW95	Q9cw95 bordetella	754	6	2.1	181	16	Q7WH22	Q7wh22 bordetella
682	6	2.1	170	16	Q7W9N5	Q7w9N5 bordetella	755	6	2.1	181	16	Q7VWEC	Q7vwe22 bordetella
683	6	2.1	171	16	Q827F9	Q827F9 streptomyc	756	6	2.1	181	16	Q93Z09	Q93z09 arabidopsis
684	6	2.1	172	5	Q81971	Q81971 plasmodium	757	6	2.1	182	10	Q93Z09	Q93z09 arabidopsis
685	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	758	6	2.1	182	16	Q7UW75	Q7UW75 rhodospirall
686	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	759	6	2.1	182	16	Q7UW75	Q7UW75 rhodospirall
687	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	760	6	2.1	183	16	Q9PQB2	Q9pgb2 ureaplasma
688	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	761	6	2.1	184	2	Q9FOS1	Q9fos1 escherichia
689	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	762	6	2.1	184	2	Q9FOS3	Q9fos3 escherichia
690	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	763	6	2.1	184	2	Q82970	Q82970 bacillus sp
691	6	2.1	172	12	Q8VBN8	Q8vbn8 thogoto vir	764	6	2.1	184	2	Q9FOS2	Q9fos2 escherichia
692	6	2.1	173	2	Q87662	Q87662 salmonella	765	6	2.1	184	2	Q47223	Q47223 escherichia
693	6	2.1	173	2	Q87662	Q87662 salmonella	766	6	2.1	184	2	Q84DV9	Q84dv9 escherichia
694	6	2.1	173	2	Q87662	Q87662 salmonella	767	6	2.1	184	2	Q84DV7	Q84dv7 escherichia
695	6	2.1	173	6	Q85L17	Q85l17 felis silve	768	6	2.1	184	2	Q84DV1	Q84dv1 escherichia
696	6	2.1	173	16	Q8FL70	Q8fl70 escherichia	769	6	2.1	185	10	Q8LBP6	Q8lbp6 arabidopsis
697	6	2.1	173	16	Q83SN8	Q83sn8 shigella fl	770	6	2.1	185	10	Q7XKGS	Q7xkgs oryza sativ
698	6	2.1	174	6	Q9GMZ9	Q9gmz9 felis silve	771	6	2.1	185	16	Q9PEZ5	Q9pez5 xyella fas
699	6	2.1	174	10	Q8GR11	Q8gr11 oryza sativ	772	6	2.1	185	16	Q88QX8	Q88qx8 mycoplasma
700	6	2.1	174	11	Q8CR26	Q8cr26 mus musculu	773	6	2.1	185	16	Q82WB4	Q82wb4 nitrosomona
701	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	774	6	2.1	185	16	Q81QH7	Q81qh7 bacillus an
702	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	775	6	2.1	185	16	Q81DI6	Q81di6 bacillus ce
703	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	776	6	2.1	186	2	Q9EUN2	Q9eun2 corynebacte
704	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	777	6	2.1	186	16	Q88FJ8	Q88fj8 pseudomonas
705	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	778	6	2.1	186	16	Q7TX03	Q7tx03 mycobacteri
706	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	779	6	2.1	187	10	Q23132	Q23132 arabidopsis
707	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	780	6	2.1	187	10	Q9LY37	Q9ly37 arabidopsis
708	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	781	6	2.1	187	10	Q3LQH6	Q3lqh6 arabidopsis
709	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	782	6	2.1	187	10	Q84S21	Q84s21 oryza sativ
710	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	783	6	2.1	187	16	Q85857	Q85857 mycobacteri
711	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	784	6	2.1	188	3	Q9HFA9	Q9hfa9 trichospora
712	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	785	6	2.1	188	9	Q9MCF1	Q9mcf1 bacteriopho
713	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	786	6	2.1	188	10	Q9LZW7	Q9lzw7 arabidopsis
714	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	787	6	2.1	188	16	Q9A5R3	Q9a5r3 caulobacter
715	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	788	6	2.1	188	16	Q8X4T5	Q8x4t5 escherichia
716	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	789	6	2.1	188	16	Q88IP8	Q88ip8 pseudomonas
717	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	790	6	2.1	188	16	Q88OX8	Q88ox8 pseudomonas
718	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	791	6	2.1	188	16	Q82CS4	Q82cs4 streptomyc
719	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	792	6	2.1	189	4	Q9SEH4	Q9sen4 homo sapien
720	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	793	6	2.1	189	12	Q9QBA8	Q9qba8 yaba monkey
721	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	794	6	2.1	189	16	Q8XRM5	Q8xrm5 raistonia s
722	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	795	6	2.1	189	16	Q8PI64	Q8pi64 xanthomonas
723	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	796	6	2.1	190	6	Q7YR89	Q7yir89 bos taurus
724	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	797	6	2.1	190	10	Q9AX56	Q9ax56 oryza sativ
725	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	798	6	2.1	190	10	Q7XHB6	Q7xhb6 oryza sativ
726	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	799	6	2.1	190	12	Q9IGU8	Q9igh8 tanapox vir
727	6	2.1	174	12	Q8JU04	Q8ju04 japanese en	800	6	2.1	190	16	Q82Q22	Q82q22 salmonella
728	6	2.1	175	2	Q9RPH8	Q9rph8 erlichia r	801	6	2.1	192	2	Q70045	Q70045 escherichia
729	6	2.1	175	6	Q81033	Q81033 bos taurus	802	6	2.1	192	10	Q7XR59	Q7xr59 oryza sativ
730	6	2.1	175	16	Q8ZAD3	Q8zad3 versinia pe	803	6	2.1	192	13	Q9W733	Q9w733 acipenser r
731	6	2.1	176	16	Q8EH11	Q8eh11 shewanella	804	6	2.1	192	16	Q8FIR6	Q8fir6 escherichia
732	6	2.1	176	16	Q7VAV3	Q7vav3 prochloroco	805	6	2.1	193	12	Q9EM12	Q9em12 bradyrhizob
733	6	2.1	177	2	Q9RQC3	Q9rgc3 zymomonas m	806	6	2.1	193	16	Q97F15	Q97f15 clostridium
734	6	2.1	177	4	Q86SM1	Q86sm1 homo sapien	807	6	2.1	193	16	Q9RXR9	Q9rxr9 deinococcus
735	6	2.1	177	10	Q9C5U9	Q9c5u9 arabidopsis	808	6	2.1	194	2	P96080	P96080 thermus aqu
736	6	2.1	177	10	Q8GVR5	Q8gvr5 oryza sativ	809	6	2.1	194	10	Q8GRX6	Q8grx6 oryza sativ
737	6	2.1	177	15	Q9IREB	Q9ieb0 human immun	810	6	2.1	195	2	Q9ZIW7	Q9ziw7 streptomyc
738	6	2.1	177	15	Q8D6H0	Q8d6h0 vibrio vuln	811	6	2.1	195	4	Q9UEF8	Q9uef8 homo sapien
739	6	2.1	178	5	Q18959	Q18959 caenorhabdi	812	6	2.1	195	10	Q9LHM8	Q9lhm8 arabidopsis
740	6	2.1	178	16	Q92PF7	Q92pf7 rhizobium m	813	6	2.1	195	10	Q9C9A5	Q9c9a5 arabidopsis
741	6	2.1	178	16	Q8ZBK1	Q8zbk1 versinia pe	814	6	2.1	195	10	Q22662	Q22662 arabidopsis
742	6	2.1	178	16	Q8FE49	Q8fe49 escherichia	815	6	2.1	195	12	Q9CQZ8	Q9cqz8 hyphantria
743	6	2.1	178	16	Q8DMP4	Q8dmp4 synecococc	816	6	2.1	195	16	Q92QX3	Q92qx3 rhizobium m
744	6	2.1	178	16	Q87IR4	Q87ir4 vibrio para	817	6	2.1	195	16	Q81R29	Q81r29 bacillus an
745	6	2.1	178	17	Q96ZY3	Q96zy3 sulfolobus	818	6	2.1	196	11	Q7INK9	Q7ink9 sciurus vul
746	6	2.1	179	5	Q9GQC6	Q9gqc6 cryptospori	819	6	2.1	196	12	Q9JFF7	Q9jff7 vaccinia vi

820	2.1	196	16	Q82052	Q82g52 streptomyc	893	6	2.1	211	16	Q8DCU3	Q8dcu3 vibrio vuln
821	2.1	197	10	Q7XP32	Q7xp32 oryza sativ	894	6	2.1	211	16	Q81QE7	Q81qe7 bacillus an
822	2.1	197	11	Q9JH90	Q9jhg0 mus musculu	895	6	2.1	211	16	Q81DF7	Q81df7 bacillus ce
823	2.1	197	15	Q8Q2H0	Q8q2h0 caprine art	896	6	2.1	211	16	Q8KNX9	Q8knx9 vibrio chol
824	2.1	197	16	Q53706	Q53706 mycobacteri	897	6	2.1	212	2	Q9REC9	Q9rep9 streptomyc
825	2.1	197	16	Q7U256	Q7u256 mycobacteri	898	6	2.1	212	2	Q84CF3	Q84cy3 gamma-prote
826	2.1	197	17	Q8U272	Q8u272 pyrococcus	899	6	2.1	212	8	Q79625	Q79625 russula ros
827	2.1	198	2	Q9F419	Q9f419 mycobacteri	900	6	2.1	212	10	Q9FTK1	Q9ftk1 oryza sativ
828	2.1	198	7	Q95HX1	Q95hx1 peromyscus	901	6	2.1	212	16	Q9KC44	Q9kc44 bacillus ha
829	2.1	198	8	Q7YB08	Q7yb08 rana sylvat	902	6	2.1	212	16	Q92FG4	Q92fg4 listeria in
830	2.1	198	8	Q7YB04	Q7yb04 rana clamit	903	6	2.1	212	16	Q9RT20	Q9rt20 deinococcus
831	2.1	198	8	Q7YB03	Q7yb03 rana septen	904	6	2.1	212	16	Q88Q17	Q88q17 pseudomonas
832	2.1	198	8	Q7YB02	Q7yb02 rana gryllo	905	6	2.1	213	2	Q8GB31	Q8gb31 pseudomonas
833	2.1	198	8	Q7YB01	Q7yb01 rana gryllo	906	6	2.1	213	10	Q9J156	Q9j156 arabisopsis
834	2.1	198	8	Q7Y827	Q7y827 rana septen	907	6	2.1	214	4	Q8TB86	Q8tb86 homo sapien
835	2.1	198	8	Q7Y7M7	Q7y7m7 rana okaloo	908	6	2.1	214	10	Q8LIW3	Q8liw3 oryza sativ
836	2.1	198	8	Q7Y7M6	Q7y7m6 rana clamit	909	6	2.1	214	10	Q8LN75	Q8ln75 oryza sativ
837	2.1	198	8	Q7Y7M5	Q7y7m5 rana okaloo	910	6	2.1	214	11	Q8BW36	Q8bw36 mus musculu
838	2.1	198	8	Q7Y7I7	Q7y7i7 rana hecksc	911	6	2.1	214	16	Q7VE65	Q7ve65 prochloroco
839	2.1	198	10	Q94F10	Q94f10 arabisopsis	912	6	2.1	215	6	Q81031	Q81031 bos taurus
840	2.1	198	10	Q9T0A6	Q9t0a6 arabisopsis	913	6	2.1	215	17	Q96Y57	Q96y57 sulfolobus
841	2.1	198	16	Q92KR4	Q92kr4 rhizobium m	914	6	2.1	216	4	Q43879	Q43879 homo sapien
842	2.1	198	16	Q8REL6	Q8rel6 fusobacteri	915	6	2.1	216	4	Q95220	Q95220 homo sapien
843	2.1	198	16	Q9RIW5	Q9riw5 streptomyc	916	6	2.1	216	10	Q9SUJ7	Q9su17 arabisopsis
844	2.1	199	4	Q9Y686	Q9y686 homo sapien	917	6	2.1	216	15	Q9IE98	Q9ie98 human immun
845	2.1	199	5	Q8XKR8	Q8mxr8 caenorhabdi	918	6	2.1	217	4	Q43888	Q43888 homo sapien
846	2.1	199	16	Q8D3Q2	Q8d3q2 vibrio vuln	919	6	2.1	217	4	Q00404	Q00404 homo sapien
847	2.1	200	4	Q9F693	Q9f693 homo sapien	920	6	2.1	217	10	Q7XXF3	Q7xxf3 oryza sativ
848	2.1	200	10	Q9LT71	Q9lt71 arabisopsis	921	6	2.1	217	10	Q7XAV2	Q7xav2 lycopersico
849	2.1	200	10	Q84S22	Q84s22 oryza sativ	922	6	2.1	217	12	Q8V5Y9	Q8v5y9 bean pod mo
850	2.1	200	10	Q9FZK5	Q9fzk5 arabisopsis	923	6	2.1	217	12	Q8V5Y7	Q8v5y7 bean pod mo
851	2.1	200	11	Q9D169	Q9d169 mus musculu	924	6	2.1	217	12	Q8V5Y5	Q8v5y5 bean pod mo
852	2.1	200	11	Q8BM86	Q8bm86 mus musculu	925	6	2.1	217	12	Q8V5Y8	Q8v5y8 bean pod mo
853	2.1	200	16	Q53746	Q53746 mycobacteri	926	6	2.1	217	12	Q8V5Y6	Q8v5y6 bean pod mo
854	2.1	200	16	Q8DU60	Q8du60 streptococ	927	6	2.1	217	12	Q8V2A0	Q8v2a0 bean pod mo
855	2.1	200	16	Q7UQJ7	Q7uqj7 rhodopirell	928	6	2.1	217	16	Q9X8C9	Q9x8c9 streptomyc
856	2.1	201	8	Q96123	Q96123 triticum ae	929	6	2.1	218	2	Q9R2J4	Q9r2j4 shigella so
857	2.1	201	10	Q24400	Q24400 triticum ae	930	6	2.1	218	4	Q725U2	Q725u2 homo sapien
858	2.1	201	16	Q98FC8	Q98fc8 rhizobium l	931	6	2.1	218	8	Q8SH37	Q8sh37 unio pictor
859	2.1	201	16	Q8YV73	Q8yv73 caenorhabdi	932	6	2.1	218	8	Q8HC62	Q8hc62 margaritif
860	2.1	201	16	Q9XAN1	Q9xan1 streptomyc	933	6	2.1	218	8	Q8HC61	Q8hc61 margaritif
861	2.1	202	10	Q8S6V5	Q8s6v5 oryza sativ	934	6	2.1	218	8	Q8HC60	Q8hc60 margaritif
862	2.1	202	16	Q7VGM4	Q7vgm4 helicobacte	935	6	2.1	218	8	Q8HC54	Q8hc54 margaritif
863	2.1	203	10	Q8W2G0	Q8w2g0 oryza sativ	936	6	2.1	218	8	Q8HB48	Q8hb48 margaritif
864	2.1	203	16	Q9RVP3	Q9rvp3 deinococcus	937	6	2.1	218	8	Q8HB28	Q8hb28 potomida li
865	2.1	203	16	Q8YQ10	Q8yq10 anabaena sp	938	6	2.1	218	10	Q48763	Q48763 arabisopsis
866	2.1	203	16	Q89KJ1	Q89kj1 bradyrhizob	939	6	2.1	218	10	Q8GYQ3	Q8gyq3 arabisopsis
867	2.1	203	16	Q82EE6	Q82ee6 streptomyc	940	6	2.1	218	10	Q7XEJ3	Q7xej3 oryza sativ
868	2.1	203	17	Q97BD1	Q97bd1 thermoplasm	941	6	2.1	218	11	Q9D5U7	Q9d5u7 mus musculu
869	2.1	204	5	P91208	P91208 caenorhabdi	942	6	2.1	218	11	Q8C647	Q8c647 mus musculu
870	2.1	204	10	Q9FG08	Q9fg08 arabisopsis	943	6	2.1	219	8	Q9MD15	Q9md15 scenedesmus
871	2.1	205	17	Q9HP29	Q9hp29 halobacteri	944	6	2.1	219	16	Q8NP22	Q8np22 corynebacte
872	2.1	206	3	Q86ZM4	Q86zm4 leptospaer	945	6	2.1	219	16	Q7VB22	Q7vb22 prochloroco
873	2.1	206	15	Q90DD4	Q90dd4 human immun	946	6	2.1	220	4	Q86W10	Q86w10 homo sapien
874	2.1	206	16	Q55727	Q55727 synchocyst	947	6	2.1	220	11	Q80WES	Q80wes rattus norv
875	2.1	207	16	Q07559	Q07559 bacillus su	948	6	2.1	220	11	Q80SV1	Q80sv1 mus musculu
876	2.1	207	16	Q7UN00	Q7un00 rhodopirell	949	6	2.1	220	12	Q8Q2N2	Q8q2n2 cowpox viru
877	2.1	208	8	Q8SFU0	Q8sfu0 pseudanodon	950	6	2.1	220	12	Q8V554	Q8v554 monkeypox v
878	2.1	208	16	Q8A781	Q8a781 bacteroides	951	6	2.1	220	12	Q80HY2	Q80hy2 vaccinia vi
879	2.1	208	16	Q8A717	Q8a717 bacteroides	952	6	2.1	220	16	Q9A5K5	Q9a5k5 caulobacter
880	2.1	208	16	Q82H13	Q82h13 streptomyc	953	6	2.1	220	16	Q8FM77	Q8fm77 corynebacte
881	2.1	209	8	Q8SK63	Q8sk63 unio timidu	954	6	2.1	220	16	Q99B33	Q99b33 buchnera ap
882	2.1	209	16	Q9KVJ9	Q9kvj9 vibrio chol	955	6	2.1	221	2	Q9ZAP4	Q9zap4 photobacter
883	2.1	209	16	Q8P3C8	Q8p3c8 xanthomonas	956	6	2.1	221	8	Q8WEU5	Q8weu5 atrina pect
884	2.1	209	16	Q89JR9	Q89jr9 bradyrhizob	957	6	2.1	221	10	Q8L8X9	Q8l8x9 arabisopsis
885	2.1	209	16	Q82GB1	Q82gb1 streptomyc	958	6	2.1	221	10	Q8C8Z9	Q8c8z9 arabisopsis
886	2.1	210	5	Q9VNN5	Q9vnn5 drosophila	959	6	2.1	221	16	Q8YCP0	Q8ycp0 bruceella me
887	2.1	210	8	Q9BA07	Q9ba07 populus tre	960	6	2.1	221	16	Q8XWR6	Q8xwr6 raietonia s
888	2.1	210	16	Q8XK36	Q8xk36 clostridium	961	6	2.1	221	16	Q833K7	Q833k7 enterococcu
889	2.1	210	16	Q8ADA8	Q8ada8 vibrio vuln	962	6	2.1	221	16	Q82AB1	Q82ab1 streptomyc
890	2.1	210	16	Q8CYU9	Q8cyu9 streptococ	963	6	2.1	222	3	O14451	O14451 cochllobolu
891	2.1	210	16	Q8CRB3	Q8ctb3 staphylococ	964	6	2.1	222	5	Q9GRE2	Q9gre2 drosophila
892	2.1	211	2	Q93R25	Q93r25 vibrio algi	965	6	2.1	222	5	Q86IWO	Q86iwo dictyosteli

966 2.1 222 10 Q8LE41
967 2.1 222 10 Q93V72
968 2.1 222 16 Q8P927
969 2.1 222 16 Q87SR7
970 2.1 222 16 Q7VVL8
971 2.1 222 16 Q7U4R9
972 2.1 223 8 Q8MEU9
973 2.1 223 8 Q8WEU1
974 2.1 223 8 Q8SR99
975 2.1 223 11 Q8K4V8
976 2.1 223 16 Q87J13
977 2.1 224 2 Q07193
978 2.1 224 4 Q0UGB2
979 2.1 224 8 Q85RC7
980 2.1 224 8 Q85RC3
981 2.1 224 8 Q85RC1
982 2.1 224 8 Q85RB5
983 2.1 224 10 Q49605
984 2.1 224 12 Q9Q0B1
985 2.1 224 16 Q98G00
986 2.1 225 8 Q9B513
987 2.1 225 8 Q85RC9
988 2.1 225 8 Q85RB7
989 2.1 225 8 Q85RA5
990 2.1 225 8 Q85RA1
991 2.1 225 8 Q85R87
992 2.1 225 16 Q81V49
993 2.1 225 16 Q81HX7
994 2.1 226 2 Q9A154
995 2.1 226 5 Q02118
996 2.1 226 5 Q44935
997 2.1 226 8 Q9TA06
998 2.1 226 8 Q9TA06
999 2.1 226 8 Q85RA9
1000 2.1 226 8 Q85R70

ALIGNMENTS

RESULT 1
Q726A6 PRELIMINARY; PRT; 290 AA.
AC Q726A6; Q726A6 (290 AA, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Inhibitory receptor IREM1.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RA "Molecular and functional characterization of IREM-1, a novel
RA inhibitory receptor expressed by myeloid cells".
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY303545; AAP57942.1; -.
KW Receptor.
SQ SEQUENCE 290 AA; 32354 MW; E9D84A6B417AA99B CRC64;

Query Match 57.2%; Score 166; DB 4; Length 290;
Best Local Similarity 99.6%; Pred. No. 1.7e-166;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTYLLFLWLSGYSIATQITPTVNGLRGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFLWLSGYSIATQITPTVNGLRGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVNTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

Db 61 DCKILVNTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VOYTIIDPAPVTOEETSSPTLGHHLNDRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VOYTIIDPAPVTOEETSSPTLGHHLNDRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGNSPEVQLPGLGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVMA 240
Db 181 MKYQQAAGNSPEVQLPGLGDLVADLTQLAGTSPRKATTKLSSAQVDQVEVEYVMA 240
QY 241 SLPKEDISYASLTGAEDEQPTVCNMG 267
Db 241 SUPKEDISYASLTGAEDEQPTVCNMG 267

RESULT 2
Q8NAF5 PRELIMINARY; PRT; 244 AA.
AC Q8NAF5; Q8NAF5 (244 AA, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein FLJ35438.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuka N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project".
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092757; BAC03966.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein_IG.
SQ SEQUENCE 244 AA; 26643 MW; 2C7C6EAD5F9C7FA5 CRC64;

Query Match 51.4%; Score 149; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLLTYLLFLWLSGYSIATQITPTVNGLRGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFLWLSGYSIATQITPTVNGLRGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVNTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVNTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VOYTIIDPAPVTOEETSSPTLGHHLNDR 149
Db 121 VOYTIIDPAPVTOEETSSPTLGHHLNDR 149

RESULT 3
Q8TDQ1 PRELIMINARY; PRT; 290 AA.
AC Q8TDQ1; Q8TDQ1 (290 AA, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 25, Last annotation update)
DE NK inhibitory receptor.

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GN NKIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Wan T., Zhang W., Cao X.;
RT "Novel human NK inhibitory receptor NKIR precursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251706; AA019099.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001986; E:EPSP_synth.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 290 AA; 32395 MW; D14FC04A047AAD10 CRC64;
Query Match 47.2%; Score 137; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.5e-136;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPELLTLYLLFWLGSYSATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTLYLLFWLGSYSATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
QY 121 VQVITDPAVPTQETSS 137
DB 121 VQVITDPAVPTQETSS 137
RESULT 4
Q6N6D0 PRELIMINARY; PRT; 194 AA.
AC Q6N6D0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CKRF35 leukocyte immunoglobulin-like receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029199; AA029199.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 194 AA; 21399 MW; 33B6AAE46F4FD6D CRC64;
Query Match 46.2%; Score 134; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 7.6e-133;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSEQ 74
DB 18 GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSEQ 77
QY 75 VKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVTQVITDPAVPTQEE 134
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DB 78 VKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVTQVITDPAVPTQEE 137
QY 135 TSSSPLTGTHLDN 148
DB 138 TSSSPLTGTHLDN 151
RESULT 5
Q7Z7I5 PRELIMINARY; PRT; 293 AA.
AC Q7Z7I5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 1.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375480; AAP42152.1; -.
KW Receptor.
SQ SEQUENCE 293 AA; 32655 MW; 66BEA2F8D3CF43E CRC64;
Query Match 41.4%; Score 120; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.9e-118;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSEQ 74
DB 18 GYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSEQ 77
QY 75 VKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVTQVITDPAVPTQEE 134
DB 78 VKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVTQVITDPAVPTQEE 137
RESULT 6
Q7Z7I4 PRELIMINARY; PRT; 165 AA.
AC Q7Z7I4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 2.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375481; AAP42153.1; -.
KW Receptor.
SQ SEQUENCE 165 AA; 18655 MW; F163D7D366063099 CRC64;
Query Match 24.5%; Score 71; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.4e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 RVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVTQVITDPAVPTQETSS 138
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Db      82 RVSICKDNQKRTFTVIMEDLMKTDADTYWCGIEKTCNDLGVTVQVTIDPAPVQETSSS 141
QY      139 PTLTGHHLNDR 149
Db      142 PTLTGHHLNDR 152

RESULT 7
Q8IX40
ID Q8IX40 PRELIMINARY; PRT; 201 AA.
AC Q8IX40
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TREM5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Colonna M.;
RT "Triggering receptor expressed on myeloid cells 5.";
RL Submitted (JCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF427618; AAN86133.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 201 AA; 22689 MW; 2B8027A488B97CAF CRC64;

Query Match 3.4%; Score 10; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 DRVSICKDNQK 87
Db      74 DRVSICKDNQK 83

RESULT 8
Q8N6D1
ID Q8N6D1 PRELIMINARY; PRT; 238 AA.
AC Q8N6D1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor, CMRF35
DE antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=Blood;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC028091; AAH28091.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27020 MW; 1E7679BE434BB8B9 CRC64;

Query Match 3.4%; Score 10; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78 DRVSICKDNQK 87
Db      74 DRVSICKDNQK 83
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Db      111 DRVSICKDNQK 120

RESULT 9
Q7WEKO
ID Q7WEKO PRELIMINARY; PRT; 472 AA.
AC Q7WEKO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative exported protein.
ON B4635.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640451; CBE34997.1; -.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51100 MW; F2B1B82BD7535DAC CRC64;

Query Match 3.1%; Score 9; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 LLVAASILLA 177
Db      10 LLVAASILLA 18

RESULT 10
Q7W381
ID Q7W381 PRELIMINARY; PRT; 472 AA.
AC Q7W381;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative exported protein.
ON BFP4165.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.;
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RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; X640435; CAE39444.1; -.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51100 MW; F2B1B82BD7535DAC CRC64;

Query Match
Best Local Similarity 3.1%; Score 9; DB 16; Length 472;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LLVAASLLA 177
DB 10 LLVAASLLA 18

RESULT 11
ID Q8S1L2 PRELIMINARY; PRT; 545 AA.
AC Q8S1L2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 22, Last annotation update)
DE P0684C02.5 protein.
GN P0684C02.5.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
RT clone:P0684C02.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP03290; BAB9049.1; -.
DR Gramene; Q8S1L2; -.
SQ SEQUENCE 545 AA; 61682 MW; 938C253D9FB90919 CRC64;

Query Match
Best Local Similarity 3.1%; Score 9; DB 10; Length 545;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVAAASL 175
DB 12 LLLVAAASL 20

RESULT 12
ID Q88CW3 PRELIMINARY; PRT; 1102 AA.
AC Q88CW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Potassium efflux system protein KefA, putative.
GN PP5067.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]_TaxID=160488;
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A., H.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

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RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AS016793; AAN70632.1; -.
DR TIGR; PF5067; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006685; MSion channel.
DR InterPro; IPR006686; MS_channel_dom.
DR InterPro; IPR006182; Ppantne_S_.
DR Pfam; PF00924; MS_channel; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; 1.
DR PROSITE; PS01246; UPF0003; 1.
KW Complete proteome.
SQ SEQUENCE 1102 AA; 122371 MW; 294E962DA96A6F00 CRC64;

Query Match
Best Local Similarity 3.1%; Score 9; DB 16; Length 1102;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TLYLLFWL 13
DB 712 TLYLLFWL 720

RESULT 13
ID Q7WTF2 PRELIMINARY; PRT; 3956 AA.
AC Q7WTF2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nana4.
GN NANA4.
OS Streptomyces nanchangensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=204925;
RN [1]_TaxID=204925;
RP SEQUENCE FROM N.A.
RC STRAIN=NS3226;
RX MEDLINE=22654646; PubMed=12770825;
RA Sun Y., Zhou X., Dong H., Tu G., Wang M., Wang B., Deng Z.;
RT "A Complete Gene Cluster from Streptomyces nanchangensis NS3226
RT Encoding Biosynthesis of the Polyether Ionophore Nanchangmycin.";
RL Chem. Biol. 10:431-441(2003).
DR EMBL; AF521085; AAP42858.1; -.
SQ SEQUENCE 3956 AA; 413394 MW; B6D961763065F9BD CRC64;

Query Match
Best Local Similarity 3.1%; Score 9; DB 2; Length 3956;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ASLTGAE 258
DB 727 ASLTGAE 735

RESULT 14
ID Q57313 PRELIMINARY; PRT; 149 AA.
AC Q57313;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2 precursor.
GN PPLA2-2.
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.

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OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Iijima N., Nasu Y., Takashima Y., Esaka M.;
RT "cDNA cloning and gene expression of phospholipase A2 isoform in the
RL hepatopancreas of red sea bream, Pagrus major.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009286; BAA23737.1; -
DR HSSP; P00593; 4BP2.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004523; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 149 POTENTIAL.
SQ SEQUENCE 149 AA; 16905 MW; 21D1BDEF1E60A75D CRC64;

Query Match 2.8%; Score 8; DB 13; Length 149;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 LLLVAASL 175
Db 7 LLLVAASL 14

RESULT 15
QJUMT0
ID QJUMT0 PRELIMINARY; PRT; 186 AA.
AC QJUMT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE IRC1c protein.
GN IRC1C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Cantoni C., Biassoni R.;
RT "IRC1 isoforms.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010102; CAB52292.1; -
DR SEQUENCE 186 AA; 20639 MW; 00D5E9379190EEEE CRC64;

Query Match 2.8%; Score 8; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 ASLLAWRM 180
Db 83 ASLLAWRM 90

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Search completed: September 16, 2004, 12:56:58
Job time : 150 secs